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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

April 22, 2003, 12:48:24 ; Search time 15.7143 Seconds (without alignments) 97.882 Million cell updates/sec US-09-674-716B-3 Run on:

81 1 RSSKSLLYKDGKTYLN 16 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	_	ø.	pa chain	e C.	pa chain pr	g.	pa cha	g	pa	g	ba	рa	pa	ht chain V	pa chain V-	pa chain	hain	ein pr	single chain Fv an	g kappa	hain V	g kappa chain V	g light chain V		g kappa chain V	g kappa chain	g kappa chain pr	g kappa chain	b
ΩI	KVMS16	KVMS51		A29775			ഗ								×		Д		S41374			•	PH1055			F3056		S2323	\$2265
% Query Match Length DB	~	<u>~</u>	120 1	٥	0	N	۳	m	_4	0	120 2													103 2					
% Query Match I	8	100.0	100.0	00	100.0				79.0	79.0				75.3	75.3	75.3	74.1							72.8					
Score	81	81	81	81	81	99	65	64	64	64	64	64	63	61	61	61	9	9	9	59	59	59	59	59	29	29	59	59	59
Result No.	1	7	m	4	G	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain V r Ig kappa chain V r	Ig light chain V r proteolytic antibo	Ig kappa chain V r Ig kappa chain - h					карра	ig Kappa Chain V r	kappa
S22902 S42266	2 PH0090 2 A55491	S41815 S40322		B25155 A28762					
	110 2								
72.8	70.4	70.4	69.1	67.9 67.9	67.9	67.9	67.9	67.9	67.9
5 6 8 8	57	57	26	22 22	55	22.0	55	55	55
30 31	332	34	36	37 38	6 6	4.4	42	43	4. 4. 4. 7.

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C. Accession: A01908
R. Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
R. Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A; Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot A; Reference number: A01908, MUID:79000273; PMID:99160
A; Accession: A01908
A; Accession: A01908
A; Accession: A01908
A; Molecule type: protein
A; Residues: 1-112 - RUD:
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This munuoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer
F; 16-95/Domain: immunoglobulin homology < IMM>
F; 23-93/Disulfide bonds: #status predicted
Ig kappa chain V region (M167) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
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Length 112; Indels 100.0%; Score 81; DB 1; I 100.0%; Pred. No. 3.1e-06; iive 0; Mismatches 0; Conservative 1 RSSKSLLYKDGKTYLN 16 Local Similarity les 16; Conserv Query Match Best Loca Matches ð

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Gaps

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24 RSSKSLLYKDGKTYLN 39 셤

RESULT 2

Ig kappa chain V region (M511) - mouse C;Species: Mus musculus (house mouse) C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000 C;Accesion: A01910 R;Appella, E.

Mol. Immunol. 17, 711-718, 1980 A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylche A;Reference number: A01910; MUID:81052016; PMID:6776396

A; Accession: A01910

A.Molecule type: protein
A.Residues: 1-113 cARP>
A.Residues: 1-113 cARP>
A.Residues: 1-113 cARP>
A.Residues: 1-113 cARP>
C.Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap, hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lactisuperfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer
F.16-95/Domain: immunoglobulin homology < IMM>
F.13-93/Disulfide bonds: #status predicted

DB 1; Length 113; 100.0%; Score 81; Query Match

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ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
R;Shlomchik, M.; A65-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
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                                                                                             C; Species: Wus pahari
C; Species: Wus pahari
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C; Accession: B2.7; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A; Title: Exolution of a V-kappa gene family.
A; Reference number: A91751; MUID:87006895; PMID:3093373
A; Accession: B29775
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-120 cJOUA
A; Cross-references: GB:ML5553; NID:g197470; PIDN:AAA39037.1; PID:g197471
A; Note: this sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840324
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
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A;Introns: 17/1
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: imtunoglobulin
C;Keywords: heteroterramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-112 < SHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heroretramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology < IMM>
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100.0%; Pred. No. 3.4e-06;
tive 0; Mismatches 0; Indels
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Pred. No. 0.00097;
4; Mismatches 0; Indels
                                                                           Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
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F;62-93/Region: framework 3
P;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%;
Matches 16; Conservative 0
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75.0%;
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24 KSSQSLLYRNGKTYLN 39
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Matches 12;
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PL0273
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CjComplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

Asin disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotetramer

CjKeywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-120/Product: Ig kappa chain V region (VKIG7) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                           Ig kappa chain precursor V region (VK167) - mouse
C;Species: Mus musculus (house mouse)
C;Accession: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C;Accession: A01909
R;Selsing, E.; Storb, U.
Cell 25, 47-58, 1981
A;Fitle: Somatic mutation of immunoglobulin light-chain variable-region genes.
A;Reference number: A01909; MUID:82002223; PMID:6791832
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <INM*
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                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A01309
A;Molecule type: DNA
A;Residues: 1-120 <SEL>
A;Note: the sequence was determined from the germline gene C;Genetics:
  100.0%; Pred. No. 3.2e-06; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Match 100.0%; Score 81; DB 1; I
Local Similarity 100.0%; Pred. No. 3.4e-06;
Ge 16; Conservative 0; Mismatches 0;
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Matches 16; Conservative
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Matches
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Ig kappa chain V region (A1) - human C; Species: Homo sapiens (man)
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Matches 12; Conservative
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44 RSSQSLVYSDGNTYLN 59
Query Match
Best Local Similarity
Matches 12; Conserv
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A;Molecule type: DNA
A;Residues: 1-120 <LAU>
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C; Superfamily: 1
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K2HURP
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SQUOUS
SQUOUS
C,Species: Mus musculus (house mouse)
C,Species: Orebel-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C,Accession: S20709
R,Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osb
Submitted to the EMBL Data Library, April 1992
A,Description: Binding specificity and variable region sequences of two monoclonal antib
A,Reference number: S20706
A,Accession: S20709
A,Accession: S20709
A,Residues: 1-111 <-RES
A,Residues: 1-111 <-RES
A,Residues: 1-111 <-RES
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sayunga chain V region - human

CiSpecies: Homo sapiens (man)

CiSpecies: Homo sapiens (man)

CiSpecies: Homo sapiens (man)

CiSpecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

CiAccession: 534095

Riwagner, S.D.; Luzzatto, L.

Bur. J. Immunol. 23, 391-397, 1993

Arities: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute

A;Reference number: 534076; MUID:93170387; PMID:8436174

A;Recession: 534095

A;Recession: 534095

A;Recession: 183 < WAG>

A;Recession: 183 < WAG>

A;Recidues: 1-83 < WAG>

A;Cross-references: EMBL:X67179

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-80/Domain: immunoglobulin homology < IMM>
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  Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: 840312; MUID:94080891; PMID:8258341
A; Accession: 840324
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-133 «KLE>
A; Cross-references: EMBL:X72434
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterctetramer; immunoglobulin homology <IMM>
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Pred. No. 0.0021;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                    Length 133;
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Pred. No. 0.0015;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                  Score 65; DB 2;
Pred. No. 0.0017;
2; Mismatches 2
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local'Similarity 75.03
Matches 12; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
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RSSQSLVYSDGNTYLN 24
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Ig kappa chain V region (A17) - human

Ig kappa chain V region (A17) - human

Ig kappa chain V region (A17) - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: April 1929 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000

C;Accession: 54226

R;Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zo A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A region A;Reference number: A49043; MUID:92201291; PMID:1551402
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: 842267
R;Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zc
Bur. J. Immunol. 22, 1023-1029, 1992
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regi
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R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin Kappa light chain genes of subgroups II and III.
A;Reference number: A93588; MUID:86041852; PMID:2997711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain precursor V-II region (RPMI) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 17/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
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75.0%; Pred. No. 0.0022;
ive 2; Mismatches 2; Indels
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Pred. No. 0.0022;
2; Mismatches 2; Indels
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Gaps

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C, Genetics:
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K2HUFR
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C;Species: Homo sapiens (man)
C;Accession: 849572
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Reference number: 849571
A;Reference number: 849571
A;Residuas: 1-114 <GIAS
A;Residuas: 1-114 <GIAS
A;Residuas: 1-114 <GIAS
A;Corosa-references: EMBL:Z46626; NID:g575261; PIDN:CAA86596.1; PID:g575262
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <INM>
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1g light chain V region (clone 17s.145) - mouse (fragment)

1g light chain V region (clone 17s.145) - mouse (fragment)

2g light chain V region (clone 17s.145) - mouse (fragment)

C, Species : Mus muscalus thouse mouse)

C, Species : Muscalus thouse mouse in the sequence revision 30-Sep-1993 #text_change 21-Jan-2000

C, Accession: PHIO57

R;Tillan, D. M. T.; Hill, R. J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c A; Reference number: PH0971; MUID:92381444; PMID:1512540

A; Accession: PH1057

A; Accession: PH1057

A; Molec:: Lype: mRNA
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A;Molecule type: DNA
A;Reaidues: 1-133 <KLO>
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 1; Length 133;
Pred. No. 0.0025;
2; Mismatches 2; Indels
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Local Similarity 75.0%;
hes 12; Conservative ;
                                                                                                                                                                  A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
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A; Introns: 17/1
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A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: A01886
R,Risesen, W.F.; Jaton, J.C.
Biochemistry 15, 3829-3833, 1976
A;Title: Variable region sequence of the light chain from a Waldenstroem's IgM with spec A;Reference number: A01886; WUID:76253627; PMID:821524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: A01886
A,Molecule type: protein
A,Residues: 1-113 <RIE>
C,Comment: This chain was isolated from a Waldenstrom's macroglobulin that binds phospho
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S.Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A01886
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A;Residues: 1-101 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reymords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                       75.3%; Score 61; DB 2; Length 101;
80.0%; Pred. No. 0.0059;
iive 2; Mismatches 1; Indels
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                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                              April 22, 2003, 12:46:53 ; Search time 8 Seconds (without alignments) 82.953 Million cell updates/sec
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                     GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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ETF_YABBAN
KV4C
ZN80_CERAE
ZN80_CERAE
ZN80_MACMU
SACB_BACCU
NIFE_METTH
YBJL_ECOLI
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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12 1 LPP 13 1 LZN 14 1 TO 14 1 TO 14 1 TO 14 1 TO 16 1 BTR 17 1 Last seq 18 1 Last seq 19 1 Last seq 10 Last seq 10 Last seq 10 Last seq 10 Last seq 10 Last seq 10 Last se	P32200 salmonella Q8zh56 yersinia pe P51503 gorilla gor P51504 homo sapien P22045 leishmania P08585 vaccinia vi P32989 variola vir P43265 euglena gra P00899 saccharomyc Q9q8k4 myxoma viru Q9q8y2 shope fibro Q03877 trypanosoma	SL	.2 AA. late) pdate)	Craniata, Vertebrata, Euteleostomi; Sciurognathi, Muridae, Murinae; Mus.	a phosphorylcholine binding	NTED FROM A MYELOMA PROTEIN THAT NCE OF THE V REGION OF THE HEAVY	FRAMEWORK-1. COMPLEMENTATITY - DETERMINING-1. COMPLEMENTARITY - DETERMINING-2. FRAMEWORK-3. FRAMEWORK-3. FRAMEWORK-4. BY SIMILARITY.	ASBEDFD6404B9726 CRC64; core 81; DB 1; Length 112; red. No. 2.7e-07; Mismatches 0; Indels 0; Gaps 0;		113 AA. update) nn update)
34	SALTY YERPE GORGO HUMAN LEIMA VACCV VARV YEAST YEAST YEAST YEAST YEAST	T I GNMEN	T; 112 nce upda ation up	aniata; iurogna	m M167,	s isolated sequence (ed.	MEWORK-1. PLEMENTARI MEWORK-2. PLEMENTARI MEWORK-3. PLEMENTARI MEWORK-3.	58EDFD6. ore 81; ed. No. Mismatcl		T; 11 nce up
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A 443 346 336 336 337 338 338 338 338 338 338 338 338 338			D; Crea Last Last gion	orda	ed=9 , regi 707(S CH OLIN S DE		349 00.0	16 39	D; Crea Last Last
A 443 346 336 336 337 338 338 338 338 338 338 338 338 338	2662 2722 2722 284 314 314 471 711		ANDARI 01, (01, 1 38, 1	a; Cho a; Roo	PubMer M. able ;	RYLCH(O BEE) 16. 16. 16.	7 1 7 1 1 1 2 2 3 3 3 3 3 4 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	12 1 vati		4NDA! 01, 01, 38,
A 443 346 336 336 337 338 338 338 338 338 338 338 338 338			ST (Rel. (Rel. (Rel.	s (Mou Metazo utheri 10090;	00273; Pottn vari tein."	ANEOUS HOSPHC AS ALS KVMS 7 IWI PRO030	11 V 10 24 40 55 55 55 55 55 55 55 55 55 55 55 55 55	112 AP 11arit Conse	LYKOGA LYKOGA	(Re (Re
	& & & & & & & & & & & & & & & & & & &		1 50SE 72A MOUSE 016Ze; 1-JUL-1986 1-JUL-1999 5-JUL-1999	us musculum ukaryota; N ammalia; Eu CBI_TaxID=1	EQUENCE. EDLINE=790(udikoff S., Kappa Chair Yeloma prot	- MISCELLI BINDS PR CHAIN HJ IR; A01908 SSP; P8036; SSP; P8036;	fam; PF000000000000000000000000000000000000	EQUENCE Y Match Local Simi	H 4	2 OUSE V2C MOUSE 01628; 1-JUL-1986 1-JUL-1996
			Ba ^l					SQ S Quer Best Matc	Oy Dp	RESULT KV2C M ID KV2C M AC P DT 2

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133 AA.

Length 120; 0; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@l8b-sib.ch).
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                                                                                                                                                                                               IG KAPPA CHAIN V-II REGION VKAPPA167.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

COMPLEMENTARITY DETERMINING-2.

FRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-3.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDILINE-86041822; PubMed=2997711; MEDILINE-86041825; PubMed=2997711; Klobeck H.G., Metndl A., Combriato G., Solomon A., Zachau H.G.; "Human immunoglobulin kappa light chain genes of subgroups II and
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63BB571F0E4DE3E8 CRC64;
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Pred. No. 3e-07;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
10-JAN-1988 (Rel. 06, Last sequence update)
10-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
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BY SIMILARITY
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                                            InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
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Local Similarity 100.0%;
les 16; Conservative 0
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PIR, A01890; K2HURP.
HSSP; P80362; 1WTL.
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InterPro; IPR003596; Ig_v.
                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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133 AA;
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P06310;
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IDD KYZP HUMAN
IDD 101-JAN
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                                                                                                                                                                                            MEDLINE-81052016; PubMed=6776396; MEDLINE-81052016; PubMed=6776396; Appella E.; Appella E.; Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein."; Mol. Immunol. 17:711-718(1980).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN THAT BINDS PROPERINE FROM A WYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kapa chain V-II region VKAPPA167 precursor.
19 kapasculus (Mouse).
19 kaparyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
19 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musina
Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-1TY.
BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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EMBL; K02415; AAA39051.1; -.
PIR; A01909; KVMS67.
HSSP; P80362; IWTL.
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Cell 25:47-58(1981).
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SEQUENCE FROM N.A.
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les 16; Conserv
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P01627;
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KV2B MOUSE
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KV2G MOUSE
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P01650; 21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1999 (Rel. 38, Last annocation update)
15-UUL-1999 (Rel. 38, Last annocation update)
15 Appa chain V-II region 7834.1.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscul-TaxID=10090;
                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Kappa chain V-II region FR.
16 Kappa chain V-II region FR.
17 Kuman).
18 Budmaryota; Mctazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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                 Length 133;
               Score 64; DB 1; Length 133
Pred. No. 0.00032;
2; Mismatches 2; Indels
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BY SIMILARITY.
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MEDLINE=83256427; PubMed=6409088;
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               79.0%;
 Query Match
Best Local Similarity 75.v.
These 12; Conservative
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24 RSSQSLVYRBGBTYLB 39
                                                                          1 RSSKSLLYKDGKTYLN 16
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                                                                                               44 RSSQSLVYSDGNTYLN 59
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113 AA;
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KV2B HUMAN
ID KV2B HUMAN
VO1615;
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Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;

"A new isotype sequence (V kappa 27) of the variable region of kappa-
"Ight chains from a mouse hybridoma-derived anti-(streptococcal group
"Ight chains from a mouse hybridoma-derived anti-(streptococcal group
"Application of the dimethylaminoszobenzene isothiocyanate reshidue."
"Application of the dimethylaminoszobenzene isothiocyanate technique
for the isolation of peptides.";

Blochem. J. 211:173-180(1983).

-!- MINECELIANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

PIRS, PRO0362; INTU.

R InterPro; IPRO03596; Ig.V.

R InterPro; IPRO03596; Ig.V.

R Pfam; PRO0404; Igy; 1.

R SMART; SMO0406; IGy; 1.

R Imminglobulin, V region; Monoclonal antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
Machino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Biochemistry 22:1153-1158(1983).";
-!- MISCELANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGGZA HYBRIDOMA PIR; A01914; KVMS26.
PROTEIN THAT BINDS DIGOXIN.
PIRSP: PRO562; JUTI.
InterPro; IPR00306; Ig.MC.
InterPro; IPR003596; Ig.W.
SMART; SW00406; Ig. No.
SMART; SW00406; IG. I.
Immunoglobulin V region; Monoclonal antibody; Hybridoma.
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21-701.

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15-701.

19 kappa chain V-II region 26-10.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordaca; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12496 MW; 42C019D10ADA3C91 CRC64;
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BY SIMILARITY.
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MEDLINE=83178921; PubMed=6404298;
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Les 11; Conservative
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113 AA;
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Query Match

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Best Loca Matches

ò 셤 RESULT 8

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Hilschmann N.; "His complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                          TISSUE=Hybridoma;
MabbinE=55128968; pubMed=6441768;
Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
Mutine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
origin: monoclonal antibodies 17529.1 and 22525.1 specific for the
group A-streptococcal polyasccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
                                                                                                           Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-II region Cum.
Howo septens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
Hischmann N.;
"Molecular hasis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
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                                                23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region 17829.1.
                 113 AA.
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BY SIMILARITY.
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HSSP, POLGO7; 1REL.
InterPro; IPRO03306; 1g_WHC.
InterPro; IPRO03596; 1g_V.
Fam; PRO047; ig; 1.
SMART; SMO0406; 1GV; 1.
Immunoglobulin V region; Hybridoma.
                 PRT;
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MEDLINE=68242259; PubMed=5586923;
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                 STANDARD;
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         KVZE MOUSE
P03976;
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KV2A_HUMAN
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MEDLINE=73166638; PubMed=470045.; Isobe T., Osserman E.F.,

Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,

Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,

Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,

Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,

Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,

J. Clin. Invest. 2.21276-1281(1973).

J. Clin. Invest. 2.21276-1281(1973).

J. Clin. Invest. 2.21276-1281(1973).

HITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

HITH THE BENCE JONES PROTEIN ISOLATED FROM THE WING OF A PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.

HISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                     Gaps
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MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
Maino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Kappa chain V.II region TEW.
Home aspiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                              66.7%; Score 54; DB 1; Length 113; 62.5%; Pred. No. 0.015; ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 53; DB 1; Length 113; larity 68.8%; Pred. No. 0.023; Conservative 2; Mismatches 3; Indels
113
12273 MW; F9F39CE949A84C2A CRC64;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones
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HSSP, A01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                Local Similarity 62.5
les 10; Conservative
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               113 AA;
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es 11; Conserv
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ID KV2D_HUMAN
AC P01617;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                     1;
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                                                                                                                                                                                       Query Match 57.4%; Score 46.5; DB 1; Length 115; Best Local Similarity 70.6%; Pred. No. 0.32; Matches 12; Conservative 1; Mismatches 3; Indels 1
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                           115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                       InterPro; IPR003066; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
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24 95 BY SIMILARITY.
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PIR; A01889; KZHUGM.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfaw; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                  1 RSSKSLLYK-DGKTYLN 16
                                                                                                                                                                                                                                                                             25 RSSQSLLDSGDGNTYLN 41
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 309:73-76(1984).
                               PIR; A01885; K2HUCM.
HSSP; P01607; 1REI.
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117 AA;
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55.6%; Score 45; DB 1; Length 117;

Query Match

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                 ö
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2288C / YP1;
MEDLINE=95308C / YP1;
MEDLINE=95304081; PubMed=7785338;
Pryde F.E., Huckle T.C., Louis B.J.;
Sequence analysis of the right end of chromosome XV in Saccharomyce cerevisiae: an insight into the structural and functional significance of sub-telomeric repeat sequences.";
Yeast 11:371-382(1995).
--- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 160 BY SIMILARITY.
247 247 MAGNESIUM (BY SIMILARITY).
296 296 MAGNESIUM (BY SIMILARITY).
321 321 MAGNESIUM (BY SIMILARITY).
437 AA; 47312 MW; 143DGEF66FB03D13 CRC64;
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                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
Enolare zerlated protein 1 (EC 4.2.1.11).
ERRI OR YMR323W OR YM9924.15.
Pred. No. 0.59;
4; Mismatches
                                                                                                                                                                     437 AA
                                                                                                                                                                     PRT;
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EMBL; U23472; AAC48992.1; -...
HSSP; P00924; 4ENL.
SGD; S0005920; ERRI.
INCEPPC; IPR000941; Enclase.
Pfam; PF00113; enclase; 1...
PROSITE; PR00146; ENCLASE.
TICRFAMS; TIGR01060; enc; 1...
PROSITE; PS00164; ENCLASE; 1...
Lyase; Glycolysis; Magnesium, ACT SITE
                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 120-437 FROM N.A.
 56.2%;
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                   9; Conservative
                                                                         28 RSSQSLLHSNGYNYLD 43
                                                                                                                                                                     STANDARD;
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                                                  1 RSSKSLLYKDGKTYLN 16
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     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                     ERR1 YEAST
P4222;
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ERR1 YEAST
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Herbat H., Chang J.Y., Aebersold R., Braun D.G.;
"Murine VK25 isotype sequence: monoclonal antibody 281.3 specific for
                                                                                                                                                                                            MEDLINE 96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            Jannabonii. ;
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 343;
Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8848EDB757FDC233 CRC64;
                                                                                                                   Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region 281.3
                                                            Last sequence update)
Last annotation update)
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                         343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                               Interpro; IPR000286; His deacetylse. Pfam; PF00850; Hist deacetyl; 1. PRINTS; PR01270; HDSAUPER. Hypothetical protein; Hydrolase; Comm. SEQUENCE 343 AA; 38174 MW; 8848EI
                         PRT;
                                                (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.9%;
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                                                  15-JUL-1998 (Rel. 36, Last 8
16-OCT-2001 (Rel. 40, Last 8
Hypothetical protein MJ0535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 69.2
9, Conservative
                         STANDARD;
                                                                                                             Methanococcus jannaschii
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                                               15-JUL-1998 (
15-JUL-1998 (
16-OCT-2001 (
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                         Y535 ME1
Q57955;
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KV2D MOUSE
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Matches
             Y535 METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
the group A streptococcal polysaccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
--- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.";
d. Bacteriol. 175:5666-5676(1993).
-!- CATALYIIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
-!- PATHWAY: Tricarboxylic acid cycle.
-!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBGNIT: MONOWER (BY SIMILARITY).
-!- MISCELLANBOUS: ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (3FE-4S) FORMS: THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THAT INTERCONVERTS CITRATE, CIS-ACONITASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mengaud J.M., Horwitz M.A., Reference of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
Aconitate hydratase (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)
(Major iron-containing protein) (MICP) (IP210).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legionella pneumophila.
Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
Legionellaceae; Legionella.
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                                                                                                                                                                                                                                                                                              FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 112;
Pred. No. 2.8;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Monoclonal DOMAIN
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MEDLINE=93374864; PubMed=8366052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.6%;
66.7%;
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HSSP; P01607; IREI.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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hes 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Matches
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DR HSSP; P16276; 1B0J.

DR InterPro; IPR001030; Aconitase C.

DR Pfan; PF00130; Aconitase I.

DR Pfan; PF001634; Aconitase C:

DR Pfan; PF00151; Aconitase C:

DR Pfan; PF00151; Aconitase C:

DR PFONO PROBLE; PR00415; Aconitase C:

DR PROSTE; PS00450; Aconitase I;

PT METAL 435 (PV SIMILARITY).

FT METAL 501 501 (RNON-SULFUR CLUSTER)

FT METAL 504 504 (IRON-SULFUR CLUSTER)

FT METAL 504 504 (IRON-SULFUR CLUSTER)

FT REAL CLUSTER)

FT REAL 500 504 (IRON-SULFUR CLUSTER)

FT REAL 500 504 (IRON-SULFUR CLUSTER)

REAL Local Similarity 69.2%; Pred. No. 28;

Matches 9; Conservative I; Mismaffches 3; Indels 0; Gaps 0;
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Search completed: April 22, 2003, 12:51:45 Job time : 9 secs

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Q8tcd0 homo sapien
Q9uB0 homo sapien
Q9c9e8 arabidopsis
Q8vci6 mus musculu
Q8yl82 mus musculu
Q8yl82 mus musculu
Q8yg37 mus musculu
Q90373 methanobact
Q91035 streptomyce
Q80779 streptomyce
Q9c926 lactococcus
Q9c926 lactococcus
Q8x0961 saccharomyc
Q8x0961 socharomyc
Q8x0961 squaromyca
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                                                                                                                                      April 22, 2003, 12:47:43 ; Search time 32 Seconds (without alignments) 103.024 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                      671580 seqs, 206047115 residues
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                                                                                              OM protein - protein search, using sw model
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Q9UL80
Q9C9E8
Q8CG16
Q9JUS2
Q8VC55
Q26451
Q99M37
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1: Sp archea:*
2: Sp bacteria:*
3: Sp fungi:*
4: Sp human:*
5: Sp invertebrate:*
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7: Sp organelle:*
7: Sp organelle:*
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Q12007
Q9P8D3
Q8X096
Q9P8F3
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Maximum Match 100%
Listing first 45 sv
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ALIGNMENTS

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Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.3%; Score 61; DB 4; Length 239; 68.8%; Pred. No. 0.029; 2; Indels :ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
Hypothetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                        QBTCDO;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
Homo sapiens (Human).
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PRT;
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Best Local Similarity 68.8
Matches 11, Conservative
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44 RSTQSLVYSDGNTYLN 59
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] -
SEQUENCE FROM N.A.
TISSUE=LUNG;
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Q9ULBO;
         QRICDO
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Q8VCI6
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09J180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 108 | 
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERAIN=CV. COLUMBIA,

MEDIANE-21016719; PubMed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federapiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federapiel N.A., Kaul S.,

Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Muhan P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.B., Cheasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Cheasy T.H., Dewar K.,

Munter J.L., Jankins J., Johnson-Hopson C., Khan S., Khaykin B.,

Langin-Hooper S., Lee A., Lee J.M., Lan S., Khaykin B.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maitt R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Maitt R., Marziali A.,

Miltecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Whiterback T., Van Aken S., Vaysberg M., Vysotekaia V.S., Walker M.,

Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu.X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myoain-reactive autoantibodies in rheumatic carditis and normal
fetus.";
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0
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MNR-2002 (TrEMBLrel. 20, Last annotation update)
170010:171
                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035034; AAD56270.1; -.
HSSP; P80360; JWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
PRam; PR00047; ig; 1.
NON_TER 1
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InterPro; IPR002052; NG Mtase.
InterPro; IPR002035; VWFA.
SM&RT; SM0327; VWR, 1.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 RSSQSPVYSDGNTYLN 39
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                                                                                                    NCBI_TaxID=9606;
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NON TER
SEQUENCE
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Q9C9E8
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MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
                                                                                                                                                                 Gapa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBL-21. 21, Last amnotation update)
01-UNN-2002 (TrEMBL-21. 21, Last amnotation update)
Hypothetical 26.2 kpa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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0
                                                                                                      Score 50; DB 10; Length 758;
Pred. No. 7.3;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitteed (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Strausberg R.;
RicerPro: IRR003599; Ig.
R InterPro: IRR003599; Ig.
R InterPro: IRR003599; Ig.
R InterPro: IRR003596; Ig.
R InterPro: IRR003596; Ig.
R Pfam; PF00047; ig. 2.
R Pfam; PF00047; ig. 2.
R SWART; SW00409; IG; 2.
R SWART; SW00409; IG; 1.
R SWART; SW00406; IGv; 1.
R SWART; SW00406; IGv; 1.
R SWART; SW00406; IGv; 1.
R PROSITE; PS00290; IG MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.5%; Score 49; DB 11; Length 238; 56.2%; Pred. No. 2.9;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin 11ght chain variable region
PROSITE; PS50234; VWPA; 1.
Hypothetical protein.
SEQUENCE 758 AA; 84789 MW; 8434F219D227036B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                               238 AA.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                            Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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les 9, Conservative
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                                                                                                                                                                                                                                                      194 SQKLIYKDGKFHLN 207
                                                                                                                                                                                                                      3 SKSLLYKDGKTYLN 16
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3 SKSLLYKDGKTYLN 16
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Matches 8; Conserv
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Best Local Similarity
FROM N.A.
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Matches
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Q9L035
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Q99M37
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
[1]
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                                                                                                                                                                                                                      59.3%; Score 48; DB 11; Length 104; 56.2%; Pred. No. 1.7; tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021781; AAH21781.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
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SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
                                                                                                                                                                                    104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA
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  Infect, Immun, 68:5803-5808 (2000).
EMBL; AF206024; AAF69322.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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Best Local Similarity 62.5
Matches 10; Conservative
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44 KSTKSLLNSDGFTYLD 59
                                                                                                                                                                                                                                                                   9; Conservative
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TISSUE=COLON;
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98 VCS S
10 O8 VCS
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MEDLINE=98037514; PubMed=9371463;

A MINTESPECTABLE TO COUCETLE-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Salith D.R., Doucette-Stamm L.A., Lumm W., Pothier B., Qiu D., Harrison D., Haarison D., Harrison D., Mierzbowski J., Gibson R., Spadafora R., Wang Y., Wierzbowski J., Gibson R., A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Ambougall S., Shimer G., Oryal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; T. Complete genome sequence of Methanobacterium thermoautotrophicum delbalt functional analysis and comparative genomics.", J. Bacteriol. 179:7135-7155 (1997).

EMBL., AE000820, AMBR487.1, T. Rice P., Mill Actual C. M., Mill Actual C. Mill Actual C. M., Mill Actual C. M., Mill Actual C. M., Mill Ac
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
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01-010-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
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PROSITE; PS0019; ACTININ_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 1561 AA; 170574 MW; 764561;
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43 RSSQSIVHSNGNTYL 57
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Q9CG26 PRELIMINARY; PRT; Q9CG26, 1rEMBLrel. 17, Created)
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ProDom; PD001568; CBD 4; 1.
SEQUENCE 574 AA; 61758 MW;
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Best Local Similarity 57.1-
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Q9CG26
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086876
006877
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DT 01-NO
DT 01-NO
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DB Alpha
GN AML.
OS Strep
OC Bacte
OC Actin
OX NCBI
RN [1]
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RR SEQUE
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MEDLINE=9700351; PubMed=8843436;
REGenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Nature 417:141-147(202).

R MSEL; A1352956; CAB88153.1; -.

R MSEP; P29957; 1AQM.

R InterPro; IPR000461; Alpha_amylase.

R InterPro; IPR00128; alpha-amylase; 1.

R Pfam; PF012806; alpha-amylase; 1.

R Pfam; PF012806; alpha-amylase; 1.

R R Pfam; PF01806; CBM_20; 1.

R PRINTS; RR0110; AAPHAAMYLASE.

R PRODOM; PD00158; CBD 4; 1.

C SEQUENCE 506 AA; 53868 MW; PCC92A3BED9D2DAE CRC64;
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STRAIN=A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chan C.W., Collins M.,
Cronin A., Praser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                              Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                     Seeger K.J, Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                            01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                         01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                        Secreted alpha-amylase.
AMLB OR SCO7020 OR SCIH10.09.
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P97179;
01-MAY-1997 (TrEMBLrel. 03, C.
D1-MAY-1997 (TrEMBLrel. 03, L.
01-JUN-2002 (TrEMBLrel. 21, L.
Alpha-amylase.
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Best Local Similarity 57.1-
8, Conservative
  PRELIMINARY;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1916;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. (VGDI_TaxID=1916;
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                                                                                       [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Subject of Guerineau M., Virolle M.J.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL; 285949; CAB06622.1; -. EMBL; 286113; CAB06815.1; -. HSSP: P29577; 1AQM. InterPro; IPR0020461; Alpha amylase.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, 1318611, CAA73926.1;
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INTERPROPTION TARM.
INTERPROPTION TO THROUGH AND A THROW.
INTERPROPTION TO THROUGH AND A THROW.
INTERPROPTION TO THROUGH AND A THROW.
PFam; PF00128; alpha-amylase C; 1.
Pfam; PF00686; alpha-amylase C; 1.
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Pfam; PF00128; alpha-amylase; 1.

Pfam; PF00286; alpha-amylase_C; 1.

Pfam; PF00686; CBM_20; 1.

PRINTS; PR00110; ALPHAANTIASE.

ProDom; P0001568; CBD 4; 1.

SEQUENCE 573 Aa; 61214 MW; R474019661C9D6A2 CRC64;
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61758 MW; A040AA1092C22270 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Query Match
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Q8X096
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MEDLINE=21235186; PubMed=11337471;
MEDLINE=21235186; PubMed=11337471;
MEDLINE=21235186; PubMed=11337471;
MEDIANE=21235186; PubMed=11337471;
Meissenbach J., Barlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sub-lactis sub-lattus Lit403.";
Genome Res. 11:731-753(2001).
EMBL; AE066360; AAX05382.1; -
InterPro; IPR00183; Decarbxy18e2.
Ffam; PF00278; Orn DAP_Arg_dec_N; 1.
Pfam; PF00278; Orn DAP_Arg_dec_N; 1.
Pfam; PF00278; Orn DAP_Arg_dec_N; 1.
PRINTS; PR01179; ODADCRBAXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Duesterhoeft A., Floeth M., Fritz M., Hilbert H., Moestl D.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).

-1- PATHWAX: GLYCOLYSIS.
-1- SUBDNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycerate hydro-lyase).

(BRR1 OR YOR393W) AND (BRR2 OR YPL281C).

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE OF 1-331 FROM N.A.
Delius H., Hebling U., Hofmann B.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delius H., Hebling U.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wambutt R., Wedler H.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
EMBL; 275301; CAA99725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA; 47279 MW; F8305C3E1FAD71E9 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Diaminopimelate decarboxylase (EC 4.1.1.20).
LYSA OR LL1284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%; Score 44; DB 16;
66.7%; Pred. No. 38;
iive 2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.3
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 RSSEVLLQEDGKTRL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 419 AA;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                               NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              012007
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-3346; TISSUE=MYCELIUM;
Nowrousian M., Kuck U., Loser K., Weltring K.M.;
Nowrousian A., Kuck U., Loser E., Weltring K.M.;
The fungal acl1 and acl2 genes encode two polypeptides with homology
to the N- and C-terminal parts of the animal ATP citrate lyase
polypeptide.,
polypeptide.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota; hungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Sordaria.
NCBI_TaxID=5147;
                                                                                                                                                                                                                                                                                                                                                                                        ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCB_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.1%; Score 43; DB 3; Length 481; 60.0%; Pred. No. 65; 4; Indels :ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                   Score 43; DB 3; Length 437;
Pred. No. 59;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 481 AA; 52240 MW; 44C93D3C4567EB28 CRC64;
                                                                                                                                                                                                                                                                                          FAF09C00BE0E711C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ATP citrate lyase, subunit 2 (EC 4.1.3.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Probable ATP citrate lyase subunit 2.
B14D6.320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                  PRINTS; PRO0148; ENOLASE.
ProDom; PD000902; Enolase; 1.
TIGREAMs; TIGR01060; eno; 1.
PROSITE; PS00164; ENOLASE; 1.
Glycolysis; Lyase; Magnesium.
SEQUENCE 437 AA; 47327 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curr. Genet. 0:0-0(0).
EMBL; AJ243817; CAB76164.1; -.
EMBL; Z73637; CAA98018.1; -.
BMBL; Z75302; CAA99728.1; -.
HSSP; P00524; 48ML.
SGD; S0005920; ERRI.
SGD; S0006292; ERRI.
InterPro; IPR000941; Enclase.
Pfam; PP00113; enclase: 1.
                                                                                                                                                                                                                                                                                                                                             53.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 SAPSVFYKDGKYDLN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SSKSLLYKDGKTYLN 16
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                                                                                                                                                                      Query Match 53.1%; Score 43; DB 3; Length 487; Best Local Similarity 60.0%; Pred. No. 66; Matches 9; Conservative 2; Mismatches 4; Indels
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAX-2000) to the EMBL/GenBank/DDBJ databases.
                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
German Neurospora,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356173; CAB91741.2; -.
Lyase.
SEQUENCE 487 AA; 52969 MW; 56BC196FCCE4CBA2 CRC64;
                                                                                                                                                                                                                                            2 SSKSLLYKDGKTYLN 16
Sarrarra
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Search completed: April 22, 2003, 12:53:45 Job time : 35 8ecs

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April 22, 2003, 12:45:19 ; Search time 40.5714 Seconds (without alignments) 52.550 Million cell updates/sec
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                             US-09-674-716B-3
81
                                                                                                                                                                                                                                                                Scoring table:
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Perfect score:
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Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

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18: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1997.DAT:*

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23: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA2000.DAT:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mouse germline kap Humanised anti-CD2 Mouse anti-CD23 MA Light chain CDR1 o Light chain of the Variable domain of Mouse MAD 2812 L c Light (kappa) chai Light chain CDR1 o Light chain CDR L1 Description AAY32254
AAE06969
AAY32262
AAY32261
AAW39818
AAW39804
AAW39804
AAW32354
AAW39815 DB Length Query Match 1000.0 1000.0 1000.0 95.1 95.1 95.1 93.8 Score 81 81 81 77 77 77 76 76

chain CD	æ) Je	Variable domain of	le don	chain	Light chain CDR1 o	Light chain of the	것	anti-	Murine anti-PAb-42	ppa lig	tide	Mouse germline kap	germline	chain of		kappa					Humanised HBV pre-	-gan	Amino acid sequenc	The kappa chain of	Insulin/insulin-li	BLyS b	chain CDF	Human Kappa II lig	ij	Peptide CDR-L1 der	Figure 11 protein	Human kappa light	Murine derived ant
AAW39824	AAW39886	AAW39801	AAW39802	AAW39803	AAW39875	AAW39839	AAW39897	AAW39805	AAY70802	AAY70790	AAE06992	AAY56670	AAE06960	AAE06961	AAW53585	AAE06993	AAE07003	AAR52057	AAU76445	AAB12170	AAB12171	AAB12173	AAY42306	AAY56735	AAY93724	AAU90900	ABP45953	AAW39821	AAU70328	AAE07007	AAY14404	AAY24099	AAE06999	AAB86292
13	13	13	19	13	13	13	13	13	21	21	22	7	22	22	19	22	52	12	21	21	21	21	20	21	21	23	23	19	23	22	20	20	22	22
16	113	113	113	113	16	16	113	114	20	122	112	93	100	100	112	112	112	113	113	113	113	113	132	133	139	247	253	15	16	112	16	112	112	16
95.6	95.6	ς.	ς.	ď	'n	ď.	85.2	85.2	82.7	ď	80.2	σ	79.0	σ	σ	79.0	g	79.0	79.0	9	79.0	79.0	9	9	79.0	σ	79.0	7	S	75.3	74.1	4	74.1	72.8
75	75	75	75	75	69	69	69	69	67	67	65	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	62.5	19	61	9	9	9	59
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

CD23, FCERII, IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; lafahimuct's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephitis; dermatitis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulttis; B-cell malignancy; therapy. Light chain CDR L1 of mouse anti-CD23 MAb C11. AAY32254 standard; Peptide; 16 AA. (first entry) Mus musculus. 15-FEB-2000

98GB-0009839. WO9958679-A1. 09-MAY-1998; 07-MAY-1999; 18-NOV-1999

(GLAX) GLAXO GROUP LTD.

N

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15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 RSSKSLLYKDGKTYLN 39
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                      WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32262;
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ID AAY3
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ZY C X X B X X B X X B X X B X X B X X B X X B X X B X X B X X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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                                                                                                                                                                                                                    This sequence represents complementarity determinating region 1 (CDR L1) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY3224-59) to render them capable of binding to the CD23 type II molecule expressed on heematopoidetic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, are used to block soluble CD23 formation for treatment of arthritis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatifis, psoriasis, unticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogrem's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis diabetes, and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; host; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                               Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 81; DB 21; Length 16; 100.0%; Pred. No. 5e-07;
  Shearin J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
  Rapson NT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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  Ellis JH,
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                                                                                                                                                                                  Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0497625.
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Crowe SJ,
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                                            WPI; 2000-053101/04.
N-PSDB; AAZ34739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 AA;
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Bonnefoy JMP,
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Matches
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The comprisions are useful for inhibiting the interaction of a call expressing CR2. They are useful for inhibiting the interaction of a call expressing CR2. They are useful for inhibiting or treating CR2 mediated disorders such as showner or inflammatory disorder, autoimmune disorders such as rheumatorid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and in the manufacture of a medicament for treating CR2-mediated classase. They are also useful for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, can discuss they are also useful for treating allergy, anaphylaxis, complicated allergic reaction, shock, seroosis, allograft rejection, ender fibrotic disease, asthma, inflammatory glomenlopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular continuency discussed in a mammal, and inhibiting narrowing of the content of a vessel in a mammal, preferably associated with vascular intervention.

CC The present sequence is mouse germline kappa light chain variable (VK) region, 167/24.
Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 81; DB 22;
100.0%; Pred. No. 3.9e-06;
ive 0; Mismatches 0;
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24..39
                                                                                                                                                                                                                                         Disclosure, Page 151; 183pp; English.
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cD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythemacosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; uxticaria; nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; sjogren's syndrome; allergy; asthma; thinitis; eczema; insulitis; graft.vergus-host disease; COPD; bronchitis; diabetes;
Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                        B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                             Mus musculus.
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                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                              Region
 This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGNYII) and the light chain complementarity determining regions (see AAY3254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides attered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, chapters, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogram's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthma, antibodies when its catchma, acute asthmatic exacerbation, rhinitis, ezema, graft-versus-host disease, CODD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly fronic bronchitis) or diabetes), and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 81; DB 21; Length 116; 100.0%; Pred. No. 4.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                 Shearin J;
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                                     'note= "framework region 2"
                                                                                                                                                                                     /note= "framework region 4"
                                                                                                               region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes, multiple sclerosis and psoriasis
                                                                                                           'note= "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining the binding agents.
                                                                          "CDR 2"
                                                                                                                              94..102
/note= "CDR 3"
   "CDR 1"
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                                                                                                                                                                                                                                                                                                      99WO-GB01434.
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                     103..113
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 /note=
40..54
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N-PSDB; AAZ34747.
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Ellis JH, Rapson NT, Shearin J;

Crowe SJ,

Location/Qualifiers "CDR L1"

55..70 /note=

/note= "CDR L2" 125..134 /note= "CDR L3"

99WO-GB01434.

98GB-0009839

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                                                                                                                                                                This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody Cl1. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAV32262 and AAV32263), which comprises sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions (see AAV32264-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble copplements in human therapy, for the treatment of arthritis, classes, uncertainty dermation, hashimoto's thyroiditis, multiple sclenosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergic asthma, intrinaic asthma, acte asthmatic exacerbation, rhinitis, ecema, graft-versue-host disease, COPD, insulitis, bronchitis (particularly chronic bernonfitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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100.0%; Pred. No. 5.8e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining the binding agents.
                                                                                                          Claim 8; Fig 2; 81pp; English.
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es 16; Conserv
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AAY32261 standard; Protein; 145 AA.

15-FEB-2000 (first entry)

AAY32261;

SAXEX

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95.1%;
                                                                                                                                      96US-0672345.
                                                                                                                 97WO-US10965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 RSSKSLLYEDGKTYLN 39
                               overdose; addiction.
                                                                                                                                                                                                   WPI; 1998-077166/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserr
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113 AA;
                                                                                                                                                                                                             N-PSDB; AAV09789
                                                                       WO9749800-A1,
                                                                                                               25-JUN-1997;
                                                                                                                                      25-JUN-1996;
                                                                                            31-DEC-1997.
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                                                                                                                                                                               Landry DW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW39804;
                                                   Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                         AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-bancoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat 60 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                         Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                  New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 19; Length 16;
Pred. No. 2.4e-06;
.; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                     Light chain CDR1 of catalytic antibody 6A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain of the catalytic antibody 2A10.
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                          AAW39818 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 81; 147pp; English.
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                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.1%;
Best Local Similarity 93.8%;
Matches 15; Conservative I
                                                                                                                                                                                                                                                   96US-0672345.
                                                                                                                                                                                                                              97WO-US10965
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSSKSLLYEDGKTYLN 16
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                                                                                                                                                                                                                                                                                                               WPI; 1998-077166/07.
                                                                                                                                          overdose; addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA;
                                                                                                                                                                                                                                                                                                                                                                    simply binding
                                                                   16-JUN-1998
                                                                                                                                                                                   WO9749800-A1
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                                                                                                                                                                                                                                                                                           Landry DW;
                                              AAW39818;
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     RESULT 5
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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were presented and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue; TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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Pred. No. 2.1e-05;
L; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 21; 147pp; English.
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Gaps
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                             The mouse VL gene product may be used to produce chimeric mouse-
human Abs against HIV-1 comprising human Ig constant regions and
murine variable regions. These novel sequence are useful in
treatment, diagnosis and prophylaxis of HIV infections, and may be
produced by a bacterial, yeast or mammalian expression system.
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                                                                                                                                                                                    93.8%; Score 76; DB 12; Length 131; 93.8%; Pred. No. 3.7e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light (kappa) chain variable region of murine 2E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric antibodies; immunoconjugates; HIV; AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                            AAR12354 standard; Protein; 132 AA.
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Matches 15; Conservative
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(GREC ) GREEN CROSS CORP.
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                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYLN 16
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                                                                                                                                                                                                                                                                                                  44 RSSKSLLYKDGKTYLS
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N-PSDB; AAQ12056.
                                                                                                                                                                                                             Local Similarity
                                                                                                                                                    131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .mmunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                            of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2AlO antibody (AAW39809 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AlO has a per minute Koat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                             AAW39801-05 represent the amino acid sequences of the variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric mouse human antibodies - used in treatment, diagnosis prophylaxis of HIV infections.
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Pred. No. 2.1e-05;
L; Mismatches 0;
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                                                                                                                                                                                                                                                                     Claim 16; Pages 73-74; 147pp; English.
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                                                  (UYCO ) UNIV COLUMBIA NEW YORK,
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            96US-0672345.
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N-PSDB; AAQ12012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AA;
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                                                                                                                                                                                                                                 simply binding
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25-JUN-1996;
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                                                                                           Landry DW;
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SXTTXBBXTXBXBXBXBXBXBXBXBXBX

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Variable domain; lambda light chain, catalytic antibody; degradation, cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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87.5%; Pred. No. 5.2e-06;
ive 2; Mismatches 0; Indels
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                                                                                                                                                                    Mus sp.
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                                                                                                                                                                                                                                                                                 Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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87.5%; Pred. No. 5.2e-06;
live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                               Light chain CDR1 of catalytic antibody 3B9.
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                                                                                                                       AAW39815 standard; peptide; 16 AA
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1 RSSKSLLYKDGKTYLN 16
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Length 16;

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AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Garalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibodies particularly for the treatment of an overdose. They are also used for treatment of an overdose. They are also used for treatming addiction (by reducing the in vivo concentration that can be
                                                                                  Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid; phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment; overdose; addiction.
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Light chain CDR1 of catalytic antibody 12H1.
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AMM39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AMM39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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87.5%; Pred. No. 4.6e-05;
ive 2; Mismatches 0; Indels
                                                                                                              Claim 12; Pages 71-72; 147pp; English.
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les 14; Conserv
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P-PSDB; AAV09791.
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Best Local Similarity
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were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6Al2 antibody (AAW19807 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6Al2 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                                                                April 22, 2003, 12:53:59 ; Search time 16.8571 Seconds (without alignments) 76.055 Million cell updates/sec
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Sequence 13, Sequence 11,
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NEO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-194-975-76

US-09-840-459-23

US-09-840-459-56

US-09-840-459-62

US-09-479-614-20

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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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81
1 RSSKSLLYKDGKTYLN 16
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Maximum DB seq length: 200000000
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Sequence 59, Appli
Sequence 6, Appli
Sequence 64, Appli
Sequence 58, Appl
Sequence 63, Appl
Sequence 1991, Ap
Sequence 78, Appl
Sequence 78, Appl
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                                                   Sequence 64,
Sequence 67,
Sequence 67,
Sequence 14,
Sequence 11,
Sequence 1,
Sequence 1,
Sequence 6,
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Sequence 6,
Sequence 7,
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Sequence 1
Sequence 1
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100.0%; Pred. No. 2.6e-06;
ive 0; Mismatches 0;
         US-09-772-120-6
US-09-840-459-54
US-09-840-459-53
US-09-840-459-63
US-09-880-748-1991
US-09-968-851-38
US-09-940-975-78
US-09-940-975-78
US-09-840-459-65
US-09-840-459-65
US-09-840-459-65
US-09-840-459-67
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US-09-840-459-67
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US-09-835-087-1
                                                                                                              US-09-809-739-11
US-09-809-739-14
US-09-809-739-15
US-09-809-739-16
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 Best Local Similarity 100.
Matches 16; Conservative
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US-09-840-459-32
 .09-840-459-32
 Query Match
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Pred. No. 0.0017;
2; Mismatches 2; Indels
                                                                                                  RESULT 5
US-10-194-975-76
US-10-194-975-76
Sequence 76, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: FOOLE, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERENCE: 50121A.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
FRIOR APPLICATION NUMBER: US 60/305,111
FRIOR PAPLICATION NUMBER: US 60/305,111
FRIOR FILING DATE: 2001-0-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patent In version 3.1
SEQ ID NO 76
LENGTH: 100
TYPE: FRT
ORGANISM: Homo sapiens
US-10-194-975-76
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US-09-840-459-23
IS-09-840-459-23
Fatent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LAROsa, GIREGOLY J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: O'Sefe, Tarran
APPLICANT: O'Brien, Slobhan H.
APPLICANT: O'Brien, Slobhan H.
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Best Local Similarity 75.0
Matches 12; Conservative
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24 RSSQSLVHSDGKTYLN 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-905-243-61
Sequence 61, Application US/09905243
Fatent No. US20020062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Immunogenicity
FILE REPERRNCE: PS0770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FateSEQ for Windows Version 3.0
SEQ ID NO 61
LENGTH: 93
                Sequence 55, Application US/09840459
Sequence 55, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION
APPLICANT: LARGBA, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HETHODS OF USE THEREPOR
FILE REFERENCE: 1865.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/20-03
PRIOR APPLICATION NUMBER: 09/21,781
PRIOR APPLICATION NUMBER: 1998-07-23
PRIOR APPLICATION NUMBER: 1998-07-23
PRIOR APPLICATION NUMBER: 109/2000-03
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ORGANISM: Macaca cynomolgus
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Matches 12, Conservative
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COCATION: (54)...(61)
COTHER INFORMATION: CDRII
US-09-905-243-61
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NAME/KEY: DOMAIN
LOCATION: (24)...(39)
OTHER INFORMATION: CDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-55
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Pred. No. 0.0017;
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Sequence 24, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LANGAGA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'SPIEN, Siobhan H.
APPLICANT: O'SPIEN, Siobhan H.
APPLICANT: O'SEIEN, Siobhan H.
APPLICANT: O'REGE, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ENGINE THEREFOR
FILE REFERENCE: 1855.105-012
CURRENT PILING DATE: 2001-02-02
PRIOR PLICATION NUMBER: US/497,625
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 1999-07-23
PRIOR PLING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SECONTAMER FARENCE ID NOS: 107
SECONTAMER FARENCE FRENCE FARENCE FOR THE FARENCE FARENC
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR PILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-03
PRIOR PILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 100
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CHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-24
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Best Local Similarity 75.0%;
Matches 12; Conservative
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24 KSSQSLLYSNGKTYLN 39
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) ORGANISM: Mus musculus
US-09-840-459-23
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24 KSSQSLLYSNGKTYLN 39

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APPLICANT: McCall.vv:
APPLICANT: McCall.vv:
APPLICANT: Weber, Exic
APPLICANT: Weber, Exic
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 1999-01-07
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 242
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Sequence 1964, Application US/09880748

Publication No. US2003065937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPRENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-33-16

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 3239

SEG ID NOS: 3239

SEG ID NOS: 3239
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Pred. No. 0.0044;
2; Mismatches 2; Indels
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Pred. No. 0.0047;
2; Mismatches 2; Indels
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Patent No. US2/0201555/6Al
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Ones, S. Tarran
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Publication No. US20030013183A1
GENERAL INFORMATION:
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Best Local Similarity 75.0'
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164 RSSQSLVYSDGNTYLN 179
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Best Local Similarity 75.0
Matches 12; Conservative
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CRCANISM: Homo sapiens
US-09-880-748-1964
                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-20
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US-09-880-748-1964
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US-09-840-459-70
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US-10-006-773-11
Sequence 11, Application US/10006773
GENERAL INFORMATION:
APPLICANT: Ounghans, Richard P.
TILLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antipring Reperson Application NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
SEQ ID NO 11
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US-09-479-614-26

i Sequence 26, Application US/09479614

publication No. US20030013183A1

GENERAL INFORMATION:

APPLICANT: WcCall, Catherine

APPLICANT: Weber, Exic

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFREENCE: P-1047

CURRENT APLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 1000-01-07

BARLIER APLICATION NUMBER: 60/115,033

SEALIER PILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOOTWARE: Patentin Ver. 2.0

SEQ ID NO 26

LENGTH: 222
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                                      Score 64; DB 10; Length 112;
Pred. No. 0.0019;
2; Mismatches 2; Indels
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US-09-479-614-20
; Sequence 20, Application US/09479614
                                          79.0%;
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Best Local Similarity 75.0
Matches 12; Conservative
                                          Query Match 79.0
Best Local Similarity 75.0
Matches 12; Conservative
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24 RASQSLLYSDGNTYLN 39
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Best Local Similarity
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; ORGANISM: Mus sp.
US-10-006-773-11
    US-09-840-459-66
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Search completed: April 22, 2003, 13:11:11 Job time : 17.8571 secs

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Pred. No. 0.006;
3; Mismatches 2; Indels
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US-09-840-459-62
i Sequence 62, Application US/09840459
patent No. US2002015057641
j GENERAL INFORMATION:
i APPLICANT: LaROSA, Gregory J.
APPLICANT: Horvath, Christopher
j APPLICANT: Naman, Walter
i APPLICANT: Ornes, S. Tarran
APPLICANT: O'Sefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PRICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR PLING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 62
LENGTH: 112
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT PELLONG DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US/9/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: DC/10801/03537
PRIOR PILING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR PLING DATE: 1999-07-22
PRIOR PLING DATE: 1998-07-23
PRIOR PLING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FASISEQ for Windows Version 3.0
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Best Local Similarity 68.8%;
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-09-840-459-62
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CORGANISM: Homo sapiens
US-09-840-459-70
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LMSTRAS 61
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KV2C MOUSE
1D KV2C MOUSE
AC P01628;
DT 21-JUL-1986 (1)
DT 15-JUL-1999 (1)
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P01626;
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KV2A MOUSE
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                                                                                                                                                                                April 22, 2003, 12:46:53 ; Search time 3.5 Seconds (without alignments) 82.953 Million cell updates/sec
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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1 LMSTRAS 7
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RAY MEDLINE=79000273; PubMed=99160;

RAY MEDLINE=79000273; PubMed=99160;

RY RADPA Chain variable region from M167, a phosphorylcholine binding

RY RADPA Chain variable region from M167, a phosphorylcholine binding

RY MASCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA PROTEIN THAT

ELINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY

CC CHAIN THAS ALSO BEEN DETERMINED.

REALS A01908; KWMS16.

DR RICA PRO0108; KWMS16.

BR HSSP; PR00360; Ig_MC.

BR INCEPPO: IPR003596; Ig_WC.

BR INCEPPO: IPR003596; Ig_V.

RIMMARY: SM00406; IGY, 1.

FT DOMAIN

40 54 FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN

52 93 FRAMEWORK-3.

FT DOMAIN

54 93 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN

55 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN

56 93 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN

57 DOMAIN

58 100 COMPLEMENTARITY-DETERMINING-3.
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           P47244 paramecium
P13341 rattus norv
P0564 saccharomyc
Q08269 saccharomyc
P55465 rhizobium s
P38164 saccharomyc
P32597 saccharomyc
Q9u525 schizosacch
Q14139 schizosacch
Q01613 xenopus lae
P08121 mus musculu
 sus scrofa
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                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 03, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Kappa chain V-II region MOPC 167.
16 Kappa chain V-II region MOPC 167.
17 Mus musculus (Mouse).
18 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12349 MW; A58EDFD6404B9726 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                              ALIGNMENTS
                              CA13 RAT
METE YEAST
ALRI YEAST
YAGI RHISN
YBK4 YEAST
STH1 YEAST
HRP1 SCHPO
HRP3 SCHPO
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CA13 MOUSE
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MEDLINE-98044031; PubMedeg384377;

RA MEDLINE-98044031; PubMedeg384377;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borries R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouillet S., Errington T.V., Commerton I.F., Cummings N.J., Daniel R.A.,

RA Entiz C., Fujter M., Fujta Y., Fuma S., Galizal A., Galleron P.T.,

RA Fritz C., Fujter M., Fujta Y., Fuma S., Galizal A., Galleron N.,

RA Ghim S.Y., Gaser P., Goffeau A., Golightly E.J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Wilser K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Koritz C., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nobeck M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nobeck M.,

RA Parro V., Poll T.M., Portetelle D., Porwollik S., Prescort A.M.,

RA Frescenn E., Pujic P., Purnelle B., Rapoport G., Schoe M., Sadaie Y.,

RA Frescenn E., Pujic P., Purnelle B., Rapoport G., Shin B.S.,

RA Gatorin J., Sekowaka A., Sero S.J., Serror P., Shin B.S., Soldo B.,

RA Freecen M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Tosaro V., Uchlyama S., Vandenbol M., Vannier F., Vassarott A.,

RA Varia A., Walbutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Walpat A., Yamamoto H., Yamane K., Yasaroto K., Yata K.,

RA Winters P., Walpat A., Yamamoto H., Yamane K., Yasaroto K., Yata K.,
                                                                                                                                                                                             IG KAPPA CHAIN V-II REGION VKAPPA167.
                                                                                                                                                                                                                   FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                            FRAMEWORK-2.
COMPLENSUTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLENSUTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 1; Length 120;
Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noback M.A., Terpstra P., Holsappel S., Venema G., Bron
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
63BB571F0B4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
15-JJJ-1998 (Rel. 36, Last sequence update)
15-JJN-2002 (Rel. 41, Last annotation update)
YHGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
InterPro; IPR003006; InterPro; IPR003006; InterPro; IPR003596; Ig_v.

Pfan; PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.
FT CHAIN 21 120 IG F
FT CHAIN 21 43 FF7

"T DOMAIN 44 59 C

"T NOMAIN 60 74

"T NOMAIN 75 81
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                113 B
                                                                                                                                                                                                                                                                                                                                                                                                            y Match 100.0%;
Local Similarity 100.0%;
hes 7; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                      120 AA;
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75 LMSTRAS 81
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P38048;
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YHGB BACSU
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                                                                                                                                                                                                                                         Appella E.;
"Mainto acid sequence of the light chain variable region of M511, a
phosphorylcholine-binding murine myeloma protein.";
Mol. Immunol. 17:711-718(1980).
-- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
PIRS, PROMSON, THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PROSPORY.
INTERPRO, KWMS1.
HSSP, PRO3506; Ig MHC.
InterPro; IPRO3506; Ig MHC.
InterPro; IPRO3506; Ig WHC.
InterPro; IPRO3506; Ig WHC.
InterPro; IPRO3506; Ig W.
SMART; SMO0406; Ig; I.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                       Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGUENCE FROM N.A. PubMed=6791832; MEDLITE=20200223; PubMed=6791832; Selsing E., Storb U.; "Somatic mutation of immunoglobulin light-chain variable-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
1g kappa chain V-II region VKAPPA167 precursor.
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Appella E.;
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RMBL; K02415; AAA39051.1; -.
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HSSP; P80362; 1WTL.
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113 AA;
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es 7; Conserv
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Enro A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wal. Y., Yelcon M., Botstein D., Davis R.W., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                    Popham D.L., Setlow P., "Cloning, nucleotide sequence, and regulation of the Bacillus subtilis paper gene, which codes for a putative class A high-molecular-weight penicillin-binding protein."; J. Bacteriol. 175:4870-4876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 25.6 kDa protein in NTF2-SRP1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.1%; Score 27; DB 1; Length 104;
85.7%; Pred. No. 3.1;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FD968 CRC64;
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                                                                                                                                                                                                                                               MEDLINE=93328693; PubMed=8335642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y14083; CAA74515.1; -. EMBL; Z99109; CAB12849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L10630; AAA71940.2; -. PIR; C40614; C40614. SubtiList; BG10426; yhgB.
                                                                                                                                                                            SEQUENCE OF 1-67 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                     Nature 390:249-256(1997).
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Matches 6; Conserv
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01-FEB-1995 (
01-OCT-1996 (
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P40011;
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YEKO YEAST
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EMBL; U18778; AAB64543.1; -.

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MEDLINE=21848401; PUDNEG=11859380;

REDLINE=21848401; PUDNEG=11859380;

ROOK V. GWilliam R., Rajlandream M.A., Lyne M., Lyne R., Stewart A.,

ROOKS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

R Collins M., Connor R., Cromin A., Davis P., Feltwell T., Fraser A.,

Collins M., Connor R., Cromin A., Davis P., Fidalgo J., Hodgson G.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Stelton J., Simmonds M., Squares R., Stevens K.,

RA Stelton J., Simmonds M., Squares R., Stevens K.,

RA Stelton J., Volkatr G., Trivey A., Walsh S.V., Warren T., Whitehead S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Mocstl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Mocstl D., Hilbert H.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., del Rey F., Benito J.,

RA Gerrutti L., Low T., Wocombie W.R., Paulsen I., Potashkin J.,

RA Gerrutti L., Low T., Wocombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

"This Grann S., Waller B., Nurse B.,

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A globular complex formation by Ndal and the other five members of
the MCM protein family in fission yeast.";
Genes Cells 2:467-479(1997).
                                                                                                                                                                                                                                                                                                                                                                      MCM7_SCHPO STANDARD; PRI; 760 AA.
075001; P87302;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA replication licensing factor mcm7 (Minichromosome maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liang D.T., Forsburg S.L.; "Fission yeast mcm7+ is an essential gene required for normal DNA
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0
                                                                                                Length 234;
                                                                                                                                               0; Indels
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SGD; S0000812; YER010C.
Hypothetical protein.
SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                             87.1%; Score 27; DB 1;
100.0%; Pred. No. 7.8;
tive 0; Mismatches
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MEDLINE=21848401; PubMed=11859360;
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                                                                              MCM7 OR SPBC25D12.03C.
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102 LMSTRA 107
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Local Similarity 100.
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NCBI_TaxID=4896;
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WIS4_SCHPO
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                                                    This SWISS-PROT entry is copyright. If is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA replication licensing factor CDC47 (Cell division control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                            EMBL; AP070481; AAC23693.1; -.
EMBL; AL031158; CAA20099.1; -.
EMBL; AL031158; CAA20099.1; -.
EMBL; AL031208; MCM.
InterPro; IPRO104208; MCM.
Pfam; PF00493; MCM; 1.
ProDom; PD001041; MCM; 1.
PROSITE; PS00847; MCM. 1; 1.
PROSITE; PS00847; MCM. 1; 1.
PROSITE; PS00847; MCM. 1; 1.
PROSITE; PS00847; MCM. 2; 1.
Transcription regulation; DNA-binding; Nuclear protein; DNA replication; Cell cycle; ATP-binding.
DNA replication; Cell cycle; ATP-binding.
NP BIND 403 410 ATP (POTENTIAL).
CONFLICT 457 457 V -> I (IN REP. 3).
SEQUENCE 76 AA; 85622 MW; 2141F8F9CB0BAA34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.1%; Score 27; DB 1; Length 760; 100.0%; Pred. No. 29; o; Indels :ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dalton S.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
  -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE MCM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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P38132;
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193 AA.

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15-UIN-2002 (Rel. 41, Created)
15-UIN-2002 (Rel. 41, Last sequence update)
15-UIN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein S3Ae.
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                             RESULT 9
RS3A SULTO
ID RS3A S
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Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galllardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sapachez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shankovski G.V., Ussery D., Barrell B.G., Nurse P.; McCombie W.R., Paulsen I., Potashkin J., Shapakovski G.V., Ussery D., Barrell B.G., Nurse P.; Mr. Hayenome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE 17. Shiozaki M., Russell P.;
Shiozaki K., Shiozaki M., Russell P.;
Shiozaki K., Shiozaki M., Russell P.;
Mosaki M., Russell P.;
Mosaki M., Russell P.;
Mosaki M., Russell P.;
Mol. Biol. Cell 8:409-419(1997).
-!- FUNCTION INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
ACTIVATED IN UNDER CONDITIONS OF HEAT SHOCK, OXIDATIVE STRESS OR
LIMITED NUTRITION. UNLIKE WINI, IT IS NOT ACTIVATED BY CHANGES IN
THE OSWOLARITY OF THE EXTRACELULIAR ENVIRONMENT. ACTIVATES THE
WISI MAP KINASE KINASE BY PHOSPHORYLATION.
-!- SIMILARITY: BELONGS TO THE SERYTHR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                             "The Mcs4 response regulator coordinately controls the stress-activated Wak1-Wis1-Sty1 MAP kinase pathway and fission yeast cell
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EMBL; X11989; CAA72716.

EMBL; X11989; CAA72716.

EMBL; N198121; AB139762.1; -.

EMBL; P24941; ICKP.

InterPro; IPR000219; Euk_pkinase.

DR ProDom; PD000001; Euk_pkinase; I.

DR ProDom; PD00001; Euk_pkinase; I.

DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.

DR PROSITE; PS00107; PROTEIN KINASE DOM; I.

DR PROSITE; PS00109; PROTEIN KINASE DOM; I.

DR PROSITE; PS011; PROTEIN KINASE ST; I.

TAANSFEASE; Serine/Lhreonine-protein kinase; ATP-binding.

DAMIN 1043 1051 ATP (BY SIMILARITY).

1043 1051 BY SIMILARITY).

1161 BY SIMILARITY.

1161 BY SIMILARITY.
                                                                                                                                                                                                                                                                           MEDLINE=97282620; PubMed=9136929;
Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K.,
Millar J.B.A.;
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SEQUENCE OF 96-1401 FROM N.A.
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                                                                                                                                                 STRAIN=JCM 10545 / 7,
MEDLINE=21456156; PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshixawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Oshima T., Kikuchi H.,
"Complete genome sequence of an aerobic thermoacidophilic
Cremarchaeon. Sulfolobus tokodaii strain?.";
-I- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Сарв
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Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
           Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
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1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AP000982; BAB65443.1;
InterPro; IPR001593; Ribosomal S3AE.
Profor, P001015; Ribosomal S3Ae; 1.
PROSTTE, P0010191; RiBOSOWAL S3AE; 1.
RIBOSOMAL SAE; PALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
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Lewis D.L., Farr C.L., Kaguni L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 71.4%;
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Sulfolobus tokodali
                                                                     NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                          SEQUENCE FROM N.A.
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142 ILSTRAS 148
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NU2M_DROME
ID _NU2M_DROME
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Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(1) chain
                                                                                                                                                                                                     [4]
SEQUENCE OF 1-56 FROM N.A.
MEDILINE-88011348; PubMed=3116271;
Clary D.O., Wolstenholme D.R.;
"Drosophila mitcochondrial DNA: conserved sequences in the A + T-rich
"Brosophila supporting evidence for a secondary structure model of the
small ribosomal RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Mol. Evol. 25:116-125(1987).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagea alpha 1(1) chain precursor.
Collagea alpha 1(1) chain precursor.
COLLAI OR COLAI.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05340; CAA26885.1; -.
EMBL; X05915; CAA29342.1; -.
PIR; A040418; QXFF2Y.
PIR; A25797; A25797.
FlyBase; FBgn0013184; Dyak\mt:ND2.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001750; Oxidored_q1.
Oxidoreductase; NAD3, UbIquinone; Mitochondrion; Transmembrane.
SEQUENCE 341 AA; 39495 MW; E6117DE50BE9D4AF CRC64;
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MEDLINE-86137403; PubMed=3841523;
Franch B.T., Lee W.-H., Maul G.G.;
Wordcocked sequence of a cDNA clone for mouse pro alpha 1(I)
collagen protein.";
Gene 39:311-312(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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85.7%; Pred. No. 22;
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                              Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R., Wolstenholme D.R., Proceophila mitochondrial DNR: a novel gene order."; Nucleic Acids Res. 10:6619-6637(1982).
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    MEDLINE=83090428; PubMed=6294611;
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Matrix Biol. 14:593-595(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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NCBI_TaxID=10090;
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Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                    "Drosophila melanogaster mitochondrial DNA, a novel organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDUINE=84041489; PubMed=6314262;
Clary D.O., Wolstenholme D.R.;
"Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in prosophila mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                          Janeare 304:234-241(1983).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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STRAIN=2117.6 I vory Coast;
STRAIN=2117.6 I vory Coast;
MEDLINE=86089137; Pubmed=3001325;
Clary D.C., Wolstenholme D.R.;
"The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code.";
J. Mol. Evol. 22:252-271(1985).
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EMBL, J01404; AAB59238.1; -.
PIR; A00419; QXFP2M.
PIYBase, FBGn0013680; mt.ND2.
InterPro; IPR001750; Oxidored_q1.
Pfan; PF00561; oxidored_q1.
Pfan; PF00561; oxidored_q1.
Stan; PF00561; oxidored_q1.
SEQUENCE 341 AA; 39773 WW; 2B8E9528C28007D8 CRC64;
"Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary fomparisons."; Insect Mol. Biol. 4:263-278(1995).
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85.7%; Pred. No. 22;
ive 0; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
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                                                                                                                                                                  SEQUENCE OF 56-341 FROM N.A.
MEDLINE=83245048; PubMed=6408489;
de Bruijn M.H.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila yakuba (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                            -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. -!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                 SEQUENCE OF 745-1130 thus.

REDLINE-8141374; PubMed-6298597;
Monson J.M., Fitedman J., McCarthy B.J.;

Monson J.M., Fitedman J., McCarthy B.J.;

"DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene:

"DNA sequence analysis of a mouse pro alpha 1;
                                                                                                                                                                                         SEQUENCE OF 1442-1453 FROM N.A.
MORDLINES BR124276, Pubmed=3340560;
MORDLINES BR124276, Pubmed=3340560;
MORDLINES BRI24276, Pubmed=3340560;
"Two mRNAs of mouse pro alpha 1(1) collagen gene differ in the size of the 3'-untranslated region.";
Nucleic Acids Res. 16:773-773 (1988).
-1- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
                                                                                                                                                                                                                                                                              (FIBRILLAR FORMING COLLAGEN).
-!- SUBUNIT: TRIMBES OF ONE ALPHA 2(1) AND TWO ALPHA 1(1) CHAINS.
-!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LICAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
                                                                                                   MEDLINE-83157109; PubMed-6219867;
Monson J.W., McCarthy B.J., "Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
"Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO1208; VFC; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
SIGNAL
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COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
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ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
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InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
                                                                            Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEL, K03029; AAA37332.1; JOINED.
EMBL; K03030; AAA3733.1; JOINED.
EMBL; K03031; AAA3733.1; JOINED.
EMBL; K03032; AAA3733.1; JOINED.
EMBL; K03033; AAA3733.1; JOINED.
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EMBL; K03035; AAA37332.1; JOINED.
PIR; A23982; A23982.
MGD; MGI:88467; COllal.
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Pfam; PF01410; COLFI; 1.
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EMBL; X15896; CAA33904.1; -.
EMBL; M14423; AAA37333.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                 Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
1182 1207 NONHELICAL REGION (C-TERMINAL).
56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
1354 1354 N-LINKED (GLCNAC. .) (POTENTIAL).
734 736 CELL ATTACHMENT SITE (POTENTIAL).
1082 1084 CELL ATTACHMENT SITE (POTENTIAL).
1450 1450 A -> V (IN REP. 5).
1453 AA; 137944 MW; 3B802E535DF81808 CRC64;
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InterPro; IPR000885; Pib collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01391; Collagen; UWF_C.
Pfam; PF013410; Collagen; 1.8.
ProDom; PF00007; Collagen; 1.
ProDom; PF00038; Pib collagen; 1.
SMART; SM00134; VWF_C.
PR051TE; PF01208; VWFC, 1.
BXtracellular matrix; Connective tissue; Repeat; Hydroxylation;
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TRIPIDE-HELICAL REGION
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL)
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COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
                                                                                                                                                                       Score 26; DB 1; Length 1453;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                           Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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TISSUE=Skin;
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SIGNAL
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Q9XS<del>J</del>7;
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Dalgleish R.;
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Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
"A comparative study of glycopeptides derived from selected
vertebrate collagens. A possible role of the carbohydrate in fibril
formation.";
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BELLINES B4270697, PubMedes661220;
Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez P.;
Myers J., Williams C., Isamirez P.;
Myers J., Williams C., Isamirez P.;
Myers J., Williams C., Amirez P.;
Myers J., Williams J., Morabito M., Morabito M.,
Mature 310:337-340(1984).
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MEDLINE-84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Elkenberry E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINES-89025644; PubMed=3178743;

MEDLINES-89025644; PubMed=3178743;

Jacomp G., Kuivanieni H., Stacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivanieni H., Etacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivanieni H., Etacey A., Shikata H., Baldwin C.T.,

Jacomp G., All Length cDNA clone for the prepro alpha 1(1)

Chain of human type I procollagen.";

Biochem. J. 253:919-922(1988).
1089 1091 CELL ATTACHMENT SITE (POTENTIAL).
1361 1361 N-LINKED (GLCNAC. . .) (POTENTIAL)
1460 Aa; 138762 MW; SBE3674D2B570697 CRC64;
                                                                                                                                                                                           ö
                                                                                                                         Length 1460;
                                                                                                                                                                                     1; Indels
                                                                                                                         Score 26, DB 1; I pred. No. 1.1e+02; 0; Mismatches 1;
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Maekeloe J.K., Raassina M., Virta A., Vuorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-71038625; PubMed=5529814; Click E.M., Bornstein P.;
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                                                                                                                             83.9%;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                             Local Similarity
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VARIANT OI-II CYS-926.
MEDLINE=88033031; PubMed=3667599;
VOGGel B.E., Minor R.R., Freund M., Prockop D.J.;
**A point mutation in a type I procollagen gene converts glycine 748 of the alpha I chain to cysteine and destabilizes the triple helix in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91184577; PubMed=2010058; Kuivaniemi H., Tromp G., Prockop D.J.; Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
associated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of disease of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
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WARIANT OI-II ARG-569.
Walsolinke-gray 202295; PubMed=3108247;
Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
"Lethal perinatal osteogenesis imperfecta due to the substitution of arginine for glycine at residue 391 of the alpha 1(I) chain of type I
                                                                                                                                                                                                                                  Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.; Regulatory elements in the first intron contribute to transcriptional control of the human alpha 1(1) collagen gene."; Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
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MEDLINE-88033098; PubMed-2822714;
ROBSOUW C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
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Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
"Lethal osteogenesis imperfecta resulting from a single nucleotide
change in one human pro alpha 1(1) collagen allele.";
Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91374476; PubMed=1895312;
Byerrs P.H., Wallis G.A., Willing M.C.;
"Osteogenesis imperfects: translation of mutation to phenotype.";
J. Med. Genet. 28:433-442(1991).
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MEDLINE-85130970; PubMed=2857713;
Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
Fine structural analysis of the human pro-alpha 1 (1) collagen promoter structure, Alul repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
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Nucleic Acids Res. 25:181-187(1997).
                                                                         Nucleic Acids Res. 16:349-349(1988)
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                                                                                                                                                        SEQUENCE OF 1-34 FROM N.A.
MEDLINE=88097389; PubMed=3480516;
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MEDLINE=97255959; PubMed=9101290;
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"Osteogeneals imperfecta. The position of substitution for glycine by cysteine in the triple helical domain of the pro alpha 1(1) chains of type I collagen determines the clinical phenotype.";
J. Clin. Invest. 84:1206-1214(1989).
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MEDIANE=90062068; PubMed=2511192;
Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
Bubsritution of serine for alpha 1(I)-glycine 844 in a severe variant of osteogenesis imperfecta minimally destabilizes the triple helix of type I procollagen. The effects of glycine substitutions on thermal stability are either position of amino acid specific.";
J. Biol. Chem. 264:19694-19699 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89255493; PubMed=2470760;
MEDLINE-89255493; PubMed=2470760;
Patterson E., Smiley E., Bonadio J.;
"RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89109573; PubMed=2913053; Constantinou C.D., Nielsen K.B., Prockop D.J.; Constantinou C.D., Nielsen K.B., Prockop D.J.; a lethal variant of osteogenesis imperfecta has a single base mutation that substitutes cysteine for glycine 904 of the alpha 1(I) chain of type I procollagen. The asymptomatic mother has an unidentified mutation producing an overmodified and unstable type I
                                                                                                   VARIANT OI-II ARG-842.
MEDIATR=8829828; PubMed=3403550;
MEDIATR=8829828; PubMed=3403550;
Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;
"Substitution of arginine for glycine~664 in the collagen alpha 1(1)
chain in lethal perinatal osteogenesis imperfecta. Demonstration of
the peptide defect by in vitro expression of the mutant cDNA.";
J. Biol. Chem. 263:11627-11630(1998).
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MEDIINE-89218628; PubMed=3244312;
Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
"A cysteine for glycine substitution at position 1017 in an alpha
1(1) chain of type I collagen in a patient with mild dominantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
BEDLINE-89380165; Pubmed-2777764.
Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
"Characterization of point mutations in the collagen COLIA1 and COLIA2 genes causing lethal perinatal osteogenesis imperfecta.";
J. Biol. Chem. 264:15809-15812(1989).
lethal variant of osteogenesis imperfecta.";
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MEDLINE=90009313; PubMed=2794057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 264:10083-10087(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inherited osteogenesis imperfecta.";
Mol. Biol. Med. 5:197-207(1988).
                                      Biol. Chem. 262:14737-14744(1987)
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MEDLINE=89308591; PubMed=2745420;
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VARIANT OI-II CYS-1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT OI-II CYS-422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          procollagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation."
RAL RATAR REPRETATION OF STANDARD STAND
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING LECTIN.

--- SUBUNIT: HOMODIMER, U-SHAPED.
--- MISCELLANEOUS: THE 4 SITES PROPOSED FOR BINDING TO CARBOHYDRATES (N-ACETYL-D-GIJUCOSAANIE) OF RECEPTOR MOLECULES ARE ON THE SURFACE OF THE AGGLUTININ MOLECULE.
--- SIMILARITY: THERE ARE THREE VARIANTS OF WGA; VARIABILITY AMONG THEM IS OBSERVED AT A TOTAL OF 10 POSITIONS.
--- SIMILARITY: CONTAINS 4 CHITIN-BINDING DOMAINS.
                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=91370843; PubMed=2491677; Smith J.J., Raikhel N.V.; "Nucleotide sequences of cDNA clones encoding wheat germ agglutinin
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolectins.";
J. Mol. Biol. 209:475-487(1989).
-!- FUNCTION: N-ACETYL-D-GLUCOSAMINE / N-ACETYL-D-NEURAMINIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wright C.S., Raikhel N.V.; Raikhel N.V.; Sequence variability in three wheat germ agglutinin isolectins: products of multiple genes in polyploid wheat."; J. Nol. Evol. 28:32-336(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structures of two wheat germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "2.2-A resolution structure analysis of two refined N-acetylneuraminyl-lactose-wheat germ agglutinin isolectin
                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Agglutinin isolectin 1 precursor (WGA1) (Isolectin A)
                                                                                                                     PRT; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE=91039324; PubMed=2231724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparison of the refined crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90064507; PubMed=2585496;
                                                                                                                                                                                                                                                                                                                                                                                                   isolectins A and D.";
Plant Mol. Biol. 13:601-603(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89279931; PubMed=2499688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biol. 215:635-651(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M25536; AAA34256.1; -.
                                                                                                                                                                                                                             Triticum aestivum (Wheat)
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S09623; S09623.
S07289; S07289.
7WGA; 15-OCT-90.
1WGC; 15-OCT-90.
2CWG; 31-JAN-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 27-197.
                                1357 LMSTEAS 1363
                                                                                                                                                                                                                                                                               Triticeae, Tritic
NCBI_TaxID=4565;
1 LMSTRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wright C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complexes."
                                                                                                                     WHEAT
                                                                                                                                      P10968;
                                                                                                     WHEAT
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PDB;
PDB;
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Gaps

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1 83.9%; Score 26; DB 1; Length 1464; Similarity 85.7%; Pred. No. 1.1e+02; 6; Conservative 0; Mismatches 1; Indels

Best Local Similarity Matches 6; Conserv

Query Match

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| Property | Property
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FT TURN 188 189

SQ SEQUENCE 212 AA; 21239 WW; EC7B6F007DDC15EB CRC64;

Query Match 80.6%; Score 25; DB 1; Length 212;

Best Local Similarity 83.3%; Pred. No. 24;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

QY 1 LMSTRA 6

Db 3 MMSTRA 8
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Search completed: April 22, 2003, 12:51:47 Job time : 5.5 secs

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April 22, 2003, 12:48:24; Search time 6.875 Seconds (without alignments) 97.882 Million cell updates/sec
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                              US-09-674-716B-5
31
                                                                                                                                                                                                                        1 LMSTRAS 7
                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                  Run on:
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283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database** :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote replication licens MAP kinase kinase hypothetical prote probable transcrip NADH2 dehydrogenas probable ponA' pro collagen alpha 1(I collagen alpha 1(I hypothetical prote Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain pre conserved hypothetical prote flagellar motor sw agglutinin isolect agglutinin isolect hypothetical prote malate synthase (E probable type II D conserved hypothet WD repeat protein protein T22H9.4 [i probable beta-keto probable beta-keto minichromosome mai dopamine receptor-Description SUMMARIES S21626 CGHU1S T51460 S09623 T05936 T26647 T39105 E88925 KVMS51 KVMS67 E69832 S50468 C81451 E86017 E91171 T39225 E95905 D96028 QXFF2Y C70791 T16198 S34027 Query Match Length DB Score Result Š.

alcohol oxidase (E	probable membrane	probable ATP-depen	rifamycin polyketi	gene MHC DQ-beta 1	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	IB1P8-4 protein [i	hypothetical prote	cytolysin II opero	emopamil-binding p	periplasmic immuno	conserved hypothet	Cof family protein	Ø
охноль	S56293	T38885	T17464	I36903	G90913	T44544	T01726	H96833	G71422	T10331	A43860	A56122	AB3319	G97904	G95033	ALIGNMENTS
-	~	N	N	N	7	8	~	7	7	7	4	~	0	~	7	
664	778	887	5069	82	144	152	164	171	171	176	190	229	250	270	270	
90.6	90.8	90.6	90.6	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	
25	25	25	25	24	24	24	24	24	24	24	24	24	24	24	24	
30	31	32	33	34	35	36	37	88	68	40	4	42	43	44	45	

RESULT 1

19 Kappa chain V region (253.1522) - mouse (fragment) Cypecies whs muccioulus (house mouse) Cypecies whs meaning thouse mouse) Cypecies whs meaning the sequence_revision 10-Peb-1989 #text_change 16-Aug-1986 Cycesesion; G30538 R:Clafilin, J.L., Berry, J. J. Immunol. 141, 4012-4019, 1988 R:Clafilin, J.L., Berry, J. Ayelecters preliminary; mucleic acid sequence not shown; not compared with conceptual tra Ayelecters preliminary; mucleic acid sequence not shown; not compared with conceptual tra Ayelecters and Ayelecters an
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1 LMSTRAS 7

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us-09-674-716b-5.op n.rpr

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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E69832; C40614
C;Accession: E69832; C40614
C;Brust, F; Ogaswara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C; Bron, S.; Brouiller, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krosqi, S.; Kumano, M.; Kuitta, K.; Lapidus, A.; Scanlon, A; Authors: Schleich, A.; Yamano, A.; Socifone, F.; Sekiguchi, J.; Schowska, A.; Scanlon, A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.F.; Danchin, A.; Akeference number: A69880; MulD:98044033; PMID:9384377
A; Residus: Preliminary; nucleic acid sequence not shown; translation not shown
A; Residuse: 1.104 <a href="mailto:kdf">kdf</a>, Schoss-references: GB:299109; GB:AL009126; NID:g2633260; PIDN:CAB12849:1; PID:e1183011, A; Bondam: D.L.; Serlow, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiPopham, D.L.; Setlow, P.
J. Bacteriol. 175, 4870-4876, 1993
A;Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpF gene A;Reference number: A40614; MUID:93328693; PMID:8335642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dypothetical protein YER010c - yeast (Saccharomyces cerevisiae)
Cypothetical protein YER010c - yeast (Saccharomyces cerevisiae)
Cypothes: Saccharomyces cerevisiae
Cybate: 28-may-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
Cybate: 28-may-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
Cybate: 28-may-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
Cybate: 28-may-1993 #sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
AyBestrator number: 850433
AyBestrator number: 850433
AyBestrator number: 850433
AyBestrator number: 850468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 2; Length 104;
Pred. No. 11;
0; Mismatches 1; Indels
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-67 <POP>
A;Cross-references: GB:L10630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LMSTRAS 7
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                                                                                                                                                                                                                                                        A Rappa chain V region (M511) - mouse C Species Mus musculus (house mouse)
C Species Mus musculus (house mouse)
C Species Mus musculus (house mouse)
C Species (10-58p-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C Accession: A01910
MOI Immunol. 17, 711-718, 1980
A) Title: Amino acid sequence of the light chain variable region of M511, a phosphorylchd A) Reference number: A01910; MUID:81052016; PMID:6776396
A) Recession: A01910
A) Molecule type: protein
A) Residues: 1-113 AAPP>
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ia C; Neywords: heterotetramer
C; Neywords: heterotetramer
F; 16-95/Domain: immunoglobulin homology < IMM>F; 21-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riselsing, E.; Storb, U.

Call 25, 47-59, 1981

A;Title: Sommatic mutation of immunoglobulin light-chain variable-region genes.

A;Reference number: A01909; WUID:82002223; PMID:6791832

A;Accession: A01909

A;Residues: 1-120 <SEL-

A;Note: the sequence was determined from the germline gene
C;Genteics: A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <AMI>
F;31-110/Product: Ig kappa chain V region (VK167) #status predicted <AMI>
F;31-115/Domain: immunoglobulin homology <AIVM>
F;43-115/Domain: immunoglobulin homology <AIVM>
F;43-115/Disulfide bonds: #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C;Accession: A01909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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; Pred. No. 1.2;
0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 7; Conservative
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Matches 7; Conserv
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| 55 LMSTRAS 61
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A; Map position: 2
C; Function:
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ses 6; Conserv
A; Residues: 1-409 < HAY>
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Best Local
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              Elagellar motor switch protein Cj0319 [imported] - Campylobacter jejuni (strain NCTC 111) CjSpecies: Campylobacter jejuni (species: Campylobacter), Campylobacter (species: Campylobacter), Campylobacter (species: Campylobacter jejuni reveals hyphylopacter: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyphylopacter: preliminary A. Residues: 1-345. PMID: 20150912; PMID: 10688204 A. Residues: L-342 cPAR A. Residues: 1-342 cPAR A. Residues: 1-348 cPAR A. 
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A;Residues: 1-409 <STO>
A;Residues: 1-409 <STO>
A;Cross-references: GB:AE005174; NID:g12518154; PIDN:AAG58601.1; GSPDB:GN00145; UWGP:Z48
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4866
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
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A; Status: preliminary
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77 MSTRAS 82
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minichromosome maintenance protein mcm7p [imported] - fission yeast (Schizosaccharomyces N;Alternate names: cell division control protein 47 homolog
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: T39991; T45282
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Churcher, Submitted to the EMBL Data Library, July 1998
A;Reference number: Z21897
A;Accession: T39991
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-760 <a href="https://documer.com/d/">LYNA</a>
A;Residues: 1-760 <a hr
A;Cross-references: GB:BA000007; PIDN:BAB37764.1; PID:g13363815; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84341
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Aug-2000
C;Accession: T16198
R;Leimbach, D.
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                                                                                                                                                                                                                                                                                                                        87.1%; Score 27; DB 2; Length 409; llarity 100.0%; Pred. No. 45; Conservative 0; Mismatches 0; Indels
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C;Superfamily: replication licensing factor MCM7; MCM homology
F;170-662/Domain: MCM homology <MCM>
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A; Reference number: Z18475
A; Reference number: T16198
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A;Molecule type: DNA
A;Residues: 1-760 <LIA>
A;Cross-references: EMBL:AF070481; PIDN:AAC23693.1
A;Experimental source: strain Sp.011
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-842 <LEI>
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100.0%; Pred. No. 85;
tive 0; Mismatches
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A; Astatus: preliminary
A; Molecule type: DNA
A; Residues: 1-12 cKUR-
A; Residues: 1-112 cKUR-
A; Experimental source: strain 1021, megaplasmid pSymb
B; Galibert, F; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federsphel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science: 233, 666-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21360234; PMID:11474104
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A;Gene: SPDB:SPAC9G1.02
A;Map position: 1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
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                                                                                                                                                           Machinase kinase kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 0.2-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T39225
R;Churcher, C.M.; Gentlas, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A;Reference number: 221837
A;Accession: T39225
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reference number: 21837
A;Molecule type: DNA
A;Cossion: T401 <CHU>
A;References: EMBL: DSPR
A;Cossion: T401 <CHU>
A;Residues: L1401 <CHU>
A;Residues: L1401 <CHU>
A;Residues: EMBL: 298763; PIDN:CABI1500.1; GSPDB:GN00066; SPDB:SPAC9GI.02
A;Experimental source: strain 972h-; cosmid c9G1
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Pred. No. 22;
2; Mismatches (
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Similarity 71.4%;
5; Conservative
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Local Similarity 85.7%;
hes 6; Conservative
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5 IMSTRSS 11
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81 LMSTRTS 87
                              300 MSTRAS 305
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A;Gene: SMb20530
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                              셤
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A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II A;Reference number: S34925; MUID:93377417; PMID:8368014
A;Molecule type: DNA A;Residues: 407-620 <802>
A;Residues: 407-620 <802>
A;Cross-references: EMBL:Z21487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)
NyAlternate names: cell division control protein CDC47; protein YBR1441; protein YBR202w
(Species: Saccharomyces cerevisiae
C;Date: 13-Aug-1999 #sequence revision
C;Accession: S34027; S46074; S34325; S56049
R;Jacquet, M. S4027; S46074; S34325; S56049
R;Jacquet, M. S4027
A;Reference number: S34022
A;Reference number: S34022
A;Reference number: BMBL: Z21487; NID:9311665; PIDN:CAA79689.1; PID:9311678
R;Bussereau, F.; Demolis, N.; Jacquet, M.;AMallet, L.
B;Bussereau, F.; Demolis, N.; Jacquet, M.;AMallet, L.
A;Reference number: S46034
A;Reference number: S46034
A;Reference number: S46034
A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 2R
C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
Component of replication licensing factor.
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribalton, S. submitted to the EMBL Data Library, September 1994
submitted to the EMBL Data Library, September 1994
A/Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation A/Description: S56049
A/Accession: S56049
A/Accession: S56049
A/Accession: S56049
A/Rocale type: DNA
A/Rocale type: DNA
A/Rocale type: DNA
A/Rocale type: DNA
A/Coss references: EMBL:U14730; NID:9608168; PIDN:AAA86309.1; PID:9608169
C/Comment: The complex of six MCM proteins is one of several proteins that must be boun phosphorylated and dissociate from the chromatin.
                                                                            A;Gene: CESP: F28B4.2
A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
C;Superfamily: CDC25-type guanine nucleotide exchange activator homology
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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                                                                                                                                                                                                                           87.1%; Score 27; DB 2; Length 842; ilarity 100.0%; Pred. No. 94; Conservative 0; Mismatches 0; Indels
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A;Gene: SGD:CDC47; MIPS:YBR202w
A;Cross-references: SGD:S0000406; MIPS:YBR202w
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Best Local Similarity
-has 6; Conserve
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A; Residues: 1-845 < BUS>
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650 MSTRAS 655
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83.9%; Score 26; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                       A;Gene: pcaQ; SMb20580
A;Genome: plasmid
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Search completed: April 22, 2003, 12:54:47 Job time : 8.875 secs

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REDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

REDLINE=20150912; PubMed=10688204;

REDLINE=20150912; PubMed=10688204;

REDLINE=20150912; PubMed=10688204;

RESPAM: Feltwell T., Holroyd S., Anderson D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Andelse K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Anderson E. Barantell B.G.;

Mitchead S., Barrell B.G.;

Mitchead S., Barrell B.G.;

Mitchead S., Barrell B.G.;

Tree als hypervariable sequences.";

Tree als hypervariable sequences.";

RASP: Q9WY63; 1QC7.

RASSP: Q9WY63; 1QC7.

RASSP: Q9WY63; 1QC7.

RASSP: Q9WY63; 1QC7.

RESP: PROJ706; FIG_Motor_Flig.

PERM: PROJ706; PIGMOTORFLG.

PERM: PROJ706; PIGMOTORFLG.

PERM: PROJ706; PIGMOTORFLG.
                                                                                                                                                                                                                                                                                   29p9c2 uncultured
                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2002 (TrEMBLrel. 21, Last annotation update)
Flagellar motor switch protein.
FLIG OK CU0319.
                                                                                                                                                                                                                                                                                                                                                                  342 AA.
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                                                                                                                                                                               Q9UT39
Q8SXA7
Q9VNI7
Q9TXN8
Q9LUQ7
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                   Q9MGN7
Q9MGN2
Q9MGL3
Q90YJ1
Q99LL6
Q69650
Q9GY27
                                                                                                                      Q8WA98
Q9LF68
Q8VKC3
                                                                                                                                                   Q9MX44
Q9F3E2
Q9XWW6
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Q8ZAR5
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QBRQG7
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                                                 PRELIMINARY;
NCBI_TaxID=197;
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  Q9PII0
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QBx5u5 escherichia
Q19852 caenorhabdi
Q9esi5 mus musculu
Q9xbp6 myxococcus
Q9xbx6 rhizoblum m
Q95xnd8 rhizoblum m
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Q95119 rhizoblum m
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                                                                  April 22, 2003, 12:47:43 ; Search time 14 Seconds (without alignments) 103.024 Million cell updates/sec
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Q9md83
Q9md83
Q9md72
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Q9b2j6
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           GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
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Q8X5U5
Q9X8U5
Q9X8U6
Q16050
Q95XR08
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Gapop 10.0 , Gapext 0.5
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sp_archea.*
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sp_invertebrate.*
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122:
143:
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176:
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                                                  OM protein
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Miyagi Y., Yamashita T., Okuda K., Mishina M., Kawamoto S., "Delphilin: A novel PDZ-containing protein associates with the GluR-delta2 subunit.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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A InterPro; IPR000651; RasGRF.

A InterPro; IPR001659; RasGRF_CDC25.

A InterPro; IPR001659; RasGRF_CDC25.

B Fam; PF00617; RasGRF; 1.

A Pfam; PF00613; RasGRF; 1.

A SMART; SM00147; RasGRF; 1.

A SMART; SM00229; RasGRF; 1.

A SMART; SM00229; RasGRF; 1.

A SMART; SM00229; RasGRF; 1.

A PROSITE; PS00720; GDS_CDC25; 1.

A PROSITE; PS00720; GDS_CDC25; 1.

A Hypothetical Protein.

A SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.1%; Score 27; DB 5; Length 860
100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0; Indels
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EMBL; AF099933; AAG31020.1; -.

HSSP; P29476; 1QAV.

MGD; MGI:2176213; Gridzip.

InterPro; IPR0013104; FH2.

InterPro; IPR001478; PDZ.

InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ERISTOL N2;
Leimbach D.;
"The Bequence of C. elegans cosmid F28B4.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 1942834; AA83583.2; -.
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0-JMR-2001 (TrEMBLrel. 16, Created)
01-MM-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
GluR-deltaz phillic-protein.
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                                   STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01217; PRICHEXTENSN. SMART; SM00498; FH2; 1.
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Best Local Similarity 100.00
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Pfam; PF00595; PDZ; 1.
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SEQUENCE FROM N.A
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XM MEDLINE=2115621; PubMed=11258796;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Xh Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterchemorrhagic Bscherichia coli

T. Complete genome comparison with a laboratory strain K-12.";

NA Res S. 12(2001).

REMBL; AR00555; BAB37764.1; -.

REMBL; AR00555; BAB37764.1; -.

REMBL; AR00556; BAB37764.1; -.

REMBL; PRO0109; Ketoacyl-synt.

Pfam; PF02109; Ketoacyl-synt.

Pfam; PF02109; Ketoacyl-synt.

REMBL; PS00106; B. KETOACXL_SYNTHASE; UNKNOWN_1.

REMBL; PROSINE; PS00606; B. KETOACXL_SYNTHASE; UNKNOWN_1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MTN-2002 (TrEMBLrel. 20, Last sequence update)
01-MTN-2002 (TrEMBLrel. 21, Last annotation update)
Putative beta-ketoacyl-ACP synthase (Putative 3-oxoacyl-(acyl-carrier-protein) synthase II).
Z4866 OR ECS4341.
Bacherichia coli 0157:H7.
Bacheria Protecobacteria; gamma subdivision; Enterobacteriaceae;
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Q19852

D Q19852

AC Q19852

DT O1-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-CT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 13, Last annotation update)
DE Hypothetical 96.1 kDa protein.

DE Hypothetical 96.1 kDa protein.

GR F2884.2.

OS Caenorhabditis elegans.

OC Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea;

OC Rhabditidae, Peloderinae, Caenorhabditis.

NRI_TAXID=6239;

RN [1]
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SEQUENCE FROM N.A.

MEDLINE=21074933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunket G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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81;
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                                                                                                                                                                                                     409 AA.
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                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=83334;
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289 MSTRAS 294
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QUESTION 2

AC QUESTION 2

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Length 860;

Gaps

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Q9XBP6

RESULT 5 Q9XBP6

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Length 112;

us-09-674-716b-5.open.rspt

88 BB

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MEDLINE=21396508; PubMed=11481431; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Corhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Colding B., Puehler A.;

Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";

Proc. Natl. Acad. Sci. U. S.A. 98:9889-9894 (2001).

EMBL; AL603643; CAC48909-1; -

EMBL; AL603643; CAC48909-1; -

ENBL; Hypothetical procein; Complete proteome.

SEQUENCE 112 AA; 11488 MW; 95FD54B0FC5CA90E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91138770; PubMed=1995349;

MEDLINE-91138770; PubMed=1995349;

A Mattra A., Bornstein P., Pentrinen R.P.;

A Mattra A., Bornstein P., Pentrinen R.P.;

"Highly conserved sequences in the 3'-untranslated region of the Col.Al gene bind cell-specific nuclear proteins.";

FEBS Lett. 279:9-13(1991).

REBIL; 864596; AAA57049.1; -.

REMBL; MS5998; AAA52049.1; -.

REMBL; MS5998; AAA52049.1; -.

REMBL; MS5998; AAA52040.1; -.

REMBL; MS5998; ACAF2040.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE-9332646; PubMed=8349697;
MEDILINE-9332646; PubMed=8349697;
MEDILINE-93325646; PubMed=8349697;

"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I)
"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I)
chain of type I collagen result in defective chain association and
produce lethal osteogenesis imperfecta.";
J. Biol. Chem. 268:18218-18225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90110490; PubMed=2295701;
Willing M.C., Cohn D.H., Byers P.H.;
Willing M.C., Cohn D.H., Byers P.H.;
"Frameshift mutation near the 3' end of the COLIA1 gene of type I collagen predicts an elongate bro alpha 1(1) chain and results in osteogeneats imperfect type I.";
J. Clin. Invest. 85:282-290(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e+02;
0; Mismatches 1; Indel8
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UON-2001 (TrEMBLrel. 17, Last annotation update)
Type I collagen PRO alpha 1(I) chain propeptide (Fragment).
                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                    Score 26; DB 16;
Pred. No. 44;
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                                                                                                                                                                                                                                                                                                    2; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
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ilarity 71.4%;
Conservative 5
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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5 IMSTRSS 11
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Matches
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Inouye S., Jain R., Ucki T., Nariya H., Xu C., Hsu M.,
Inouye S., Jain R., Ucki T., Inouye M.;
Mwnoz-Dorado J., Farez-Vidal E., Inouye M.;
"Sequence Analysis of 13 Bukaryotic-like Protein Ser/Thr Kinases of
Myxococous xanthus, a Developmental Bacterium and Significance of
Myxocococous xanthus, brotein His Kinases.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF150691, AAD42856.1;
InterPro, IPR000149; Euk pkinase.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RB0509.
RB0509 OR SMB20530.
RB0509 OR SMB20530.
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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0
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                                                                                                      Score 27; DB 11; Length 1024; Pred. No. 1.9e+02; 1; Mismatches 0; Indels 0
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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Pfam; PF000515; TPR; 5.
ProDom: PD000001; Euk_pkinase; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;
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                     SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 1024 AA; 112578 MW; E318AFDEE02F846A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JIN-2002 (TrEMBLrel. 21, Last annotation update)
Serine/threonine kinase PKN8
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                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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53 LVSTRAS 59
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Gaps

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RESULT 6 Q92W36

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KW Plasmid, Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 33832 MW; 4787BC1BE5476709 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                         199 LMPTRAS 205
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WREDINE=21395608; PubMed=11481431;
WREDINE=21395608; PubMed=11481431;
WREDINE=21395608; PubMed=11481431;
WREDINE=21395608; PubMed=1481431;
WREDINE=21395608; PubMed=2130508;
WREDINE=21395608; PubMed=2.40cas I., Becker A., Cowie A., Gouzy J., RA Golding B., Puehler A.;
Warhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., RA Golding B., Puehler A.;
Warner complete sequence of the 1,683-kb pSymB megaplasmid from the N2-RIA and Complete sequence of the 1,683-kb pSymB megaplasmid from the N2-RIA and SymB medaymbiont Sinorhizobium melliloti."

Proc. Natl. Accode77; CAC49892.1;
DR Proc. Natl. Accode77; HTH LyR.
DR InterPro; IPRO05119; LyRR subst.
DR Pfam; PFO0126; LYRR substrate; 1.
DR Pfam; PFO0126; LYRR substrate; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative transcriptional activator of the pca operon, LysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid Byymb (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Grosse-Hovest L., Brem G.;
Grosse-Hovest L., Brem G.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ31210; CAC38832.1;
EMBL; AJ312110; CAC38832.1;
EMBL; AJ312112; CAC38832.1; JOINED.
EMBL; AJ312112; CAC38832.1; JOINED.
InterPro; IPRO00087; Collagen.
InterPro; IPRO00085; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 83.9%; Score 26; DB 6; Length 287; Local Similarity 85.7%; Pred. No. 1.16+02; nes 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 287 AA; 31698 MW; A9122CAEB7DC3DAE CRC64;
                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Pro alpha 1(1) collagen (Fragment).
                                                                                                                                        287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002078; Fib_collagen_C; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAQ OR RB1492 OR SMB20580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LMSTEAS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                        095ND8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92TL9
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Matches
                                                                      RESULT 8
10 955N08
10 955N08
10 955N08
10 1-D)
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Cochliomyia.
NCBI _TaxID=115425;
                                                                              Gaps
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MEDLINE=20485491; PrbMed=11029671;
Lessinger A.C., Martins Junqueira A.C., Lemos T.A., Kemper E.L.,
da Silva F.R., Vettore A.L., Arrada P., Azeredo-Espin A.M.;
"The mitochondrial genome of the primary screwworm fly Cochliomyia hominivorax (Diptera: Calliphoridae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEDGENCE FROM N.A.

A Lu Z., Laptev A.V., Prockop D.J.;

Lu Z., Laptev A.V., Prockop D.J.;

Lu Z., Laptev A.V., Prockop D.J.;

Lu mithe nutleoided sequence of conk for the last 5 exons and 3'-

untranalated region of murine type I(1) procollagen.";

Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

R MGDJ, MGJ188467; Collagen.

R MGDJ, MGJ188467; Collagen.

R Pfam, PF01401, COLEI; 1.

R Pfam, PF01401, COLEI; 1.

R Prochom; PD002078; Fib_collagen_C; 1.

R Prochom; PD002078; Fib_collagen_C; 1.
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       Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE 325 AA; 35229 MW; A5A21E74DFDE3EF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha-1 type I procollagen (Fragment).
COLIA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
NADH subunit 2.
Query Match 83.9%; Score 26; DB 16; Best Local Similarity 85.7%; Pred. No. 1.2e+02; Matches 6; Congervative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cochliomyia hominivorax (Primary screw-worm).
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Gaps

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7240;
                                                                                                                             MEDLINE=20225/5/; PubMed=10762421;
Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.;
Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.;
The complete sequence of the mitochondrial genome of the Medfly,
Ceratitis capitata.";
Insect Mol. Biol. 9:139-144(2000).
Insect Mol. Biol. 9:139-144(2000).
EMBL; AJ242872; CAB45088.1; -.
InterPro; IPR001750; Oxidored_q1.
Mitochondrion; NAD; Oxidored_q1; 1.
Mitochondrion; NAD; Oxidored_q1; 1.
Mitochondrion; NAD; Oxidored_c1: Biol. Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 85.7%; Pred. No. 1.3e+02; 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.9%; Score 26; DB 8; Length 341
85.7%; Pred. No. 1.38+02;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBLE, ALEGONO12889; DSIM/nt:ND2.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1.
Pfam; PF00361; oxidored_q1; I.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 341 AA; 39734 MW; 8C42C96FF977A173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=RU35, C167, DSW, DSR, MD106, MD225, AND SC00;
Ballard J.W.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 2.
Drosophila simulans (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 AA
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF200845; AAF77447.1; EMBL; AF200839; AAF77382.1; EMBL; AF200840; AAF77382.1; EMBL; AF200841; AAF77395.1; EMBL; AF200842; AAF77408.1; EMBL; AF200843; AAF77421.1; EMBL; AF200844; AAF77434.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MD83 PRELIMINARY;
Q9MD83;
01-OCT-2000 (TEMBLrel. 15,
01-OCT-2000 (TEMBLrel. 15,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LMSTEAS 57
                                                 NCBI_TaxID=7213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 LMSTEAS 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Chrysomya.
NCbl_TaxID=142978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Lessinger A.C., Junqueira A.C.M., Lemos T.A., Kemper B.L.,
Vetrore A.L., da Silva F.R., Arruda P., Azeredo-Espin A.M.L.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.9%; Score 26; DB 8; Length 338;
85.7%; Pred. No. 1.2e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 85.7%; Pred. No. 1.2e+02; 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERM; PF00361; oxidored g1; 1.
PRINTS; PR01436; NADHDHGNASE2.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 338 AA; 39228 MW; ABD5B1B5A5A46A23 CRC64;
                                                                                                                                                                                                                                                              EMBL; AF260826; AAF78613.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 338 AA; 39337 MW; E6901A86D02439D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
01-NAV-1999 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase (ubiquinone) chain 2 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created) ______Last sequence update)
Last annotation.update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ceratitis capitata (Mediterranean fruit fly). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF352790; AAK21318.1; -.
InterPro; IPR003917; NADHub_oxred2.
InterPro; IPR001750; Oxidored_q1.
                  Insect Mol. Biol. 9:521-529(2000)
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01-JUN-2001 (TrEMBLrel. 17;
01-JUN-2001 (TrEMBLrel. 17;
01-MAR-2002 (TrEMBLrel. 20;
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Propionibacterium Propionibacterium Mouse MAD 2E12 L C Light (kappa) Chai Human reproductive Escherichia coli p Propionibacterium Purphide #554 encod Protein #545 encod Human brain expres Human bone marrow Peptide #567 encod Peptide #567 encod Peptide #576 encod Human peptide encod Human peptide #567 encod Peptide #576 encod Human peptide encod Human peptide encod Human peptide #567 encod Human peptide encod Pro-alphal(I) chai

ABB18546 AAM53875 ABB33078

Scoring table:

Run on:

Total number Searched:

Database

ABB52717 ABB27906

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Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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AAU54742
AAR12232
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AAR12356
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AAM14133
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AAW12845
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ALIGNMENTS

New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required

(UYCO) UNIV COLUMBIA NEW YORK

WPI; 1998-077166/07.

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Human colon cancer

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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.01. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibodies particularly for the treatment of an overdose. They are used particularly for the treatment of an overdose. They are also used for achieved).
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iive 0; Mismatches 0;
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                                                                               AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6Al2, which is able to degrade cocarine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6Al2 antibody was identified using TSAl, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6Al2 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to relbase 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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 smaller doses than antibodies that antagonise cocaine by
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                                                   Claim 13; Page 81; 147pp; English.
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antibody C11 (see also AAY32262). The invention provides altered antibody C11 (see also AAY32262). The invention provides altered antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY3224-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies of type II molecule expressed on haematopoietic cells. The antibodies of type II molecule expressed on haematopoietic cells. The antibodies of type II molecule expressed on haematopoietic cells. The antibodies of type II molecule expressed on haematopoietic cells. The antibodies of diabetes, vieitis, dermatitis, psoriasis, untitaring achemia, antibule CD23 formation for treatment of arthritis, clohn's disease, Sjogren's syndrome, allergies, allergic achima, intrinsic asthma, southe asthmatic exacerbation, rhinitis, collitis, crohn's disease, Sjogren's syndrome, allergies, allergic achima, intrinsic asthma, acute asthmatic exacerbation, rhinitis, coming interning bronchitis) or plabetes (particularly chronic Dronchitis) or plabetes (particularly thornic Dronchitis) or plabetes (particularly the bronch Dronchitis) or plabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; conplementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                         urticaria; nephrotic syndrome; glomerulonephritis;
inflammatory bowel disease; ulcerative colitis; Crohn's disease;
Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes;
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                                                                                                                                                                                                                                                                                      Light chain CDR L2 of mouse anti-CD23 MAb C11.
                                                                                                                                                       AAY32255 standard; Peptide; 7 AA.
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LMSTRAS 7
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Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytosteatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                   O'Brien S, O'Keefe T;
                                                                                               Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                                    Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 151; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Larosa GJ, Horvath C, Newman W,
                       AAE06969 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                            02-FEB-2001; 2001WO-US03537.
                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0497625.
                                                                           (first entry)
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                                                 AAE06969;
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RESULT 5
               AAE06969
                                      monoclonal antibody; C11; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Crowe SJ, Ellis JH, Rapson NT, Shearin J;
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The patent discloses a humanised antibody or its antigen-binding for fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunospolubulin of human origin. The chumanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CCC leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatory disorder, autoimmune disorders such as rheumatory disorder, autoimmune disorders such as rheumatory disorder, autoimmune disorders such as rheurists and multiple socierosis, atherogenesis and atherosocierosis, anthibiting restenosis. They are useful in therapy or disorder and in the manufacture of a medicament for treating CCR2 mediated disorder and in the manufacture of a medicament for treating allersy, anaphylaxis, an anignanary, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, including angioplasty and/or stent placement in a mammal. The restending angioplasty and/or stent placement in a mammal. The preferably associated with vascular intervention, including angioplasty and/or stent placement in a mammal, and inhibiting nearowing of the lumanised antibodies are also useful for inhibiting nearowing of the a vessel in a mammal, and inhibiting nearowing of the region, 167/24.

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100.0%; Score 31; DB 21; Length 7; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 7; Conservative

Query Match

Sequence Query Match

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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
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                                                                                                                                              Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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                                                                                                            Light chain of the catalytic antibody 2A10.
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AAW39882 standard; Protein; 113 AA.
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N-PSDB; AAV09789.
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                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue; TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment,
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                                 DB 22; Length 100; 5.8;
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                                                                                                                                                                                                                                              AAW39886 standard; Protein; 113 AA.
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llarity 100.0%;
Conservative 0
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overdose; addiction.
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100 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                                                                                New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                    WPI; 1998-077166/07.
P-PSDB; AAV09802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA;
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                                              Landry DW;
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09-MAY-1998;
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Region
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                   AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occanie. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Stralytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The ZALO antibody (AAW39809 represents the heavy chain) was identified using TSAL, which is an immunogenic conjugate of a phosphate monoseter transition state analogue. Antibody ZALO has a per minute Kcat of 0.01. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; uxticaxia; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft.versus-host disease; COPD; bronchitis; diabetes;
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                                                                                                                                                                                                             100.0%; Score 31; DB 19; Length 113; 100.0%; Pred. No. 6.6; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-CD23 MAb C11 light chain variable region.
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/note= "framework region 4"
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Claim 16; Pages 73-74; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                             AAY32262 standard; Protein; 116 AA.
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94..102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CDR 1"
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                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                        Seguence 113 AA;
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                                                                                                                                                                  be achieved).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    AAY32262;
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Region
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This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGKVII) and the light chain complementarity determining regions (see AAV3254-56) of murine antibody C11. The altered antibodies, work as chain complementarity the invention provides attered antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them comparise of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, cups exprhementarity dermaticis, pryne II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies allergies asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eccema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly chronic bronchitis) or diabetes (particularly the main allergies allergies for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                  Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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/note= "CDR L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Fig 3; 81pp; English.
98GB-0009839.
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Matches 7, Conservative
                                                                                   (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                           WPI; 2000-053101/04.
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                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ34747.
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Region Region

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AAM39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                     New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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85.7%; Pred. No. 7.8e+05;
iive 1; Mismatches 0;
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                                                                                                                                                                            (UYCO ) UNIV COLUMBIA NEW YORK
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                                                                                                                                                                                                                                                                 WPI; 1998-077166/07.
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WO9749800-A1.
                                                                                       25-JUN-1997;
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                                            31-DEC-1997
                                                                                                                                                                                                                           Landry DW;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody Cll. The invention provides altered antibodies, such as chimerioc rhumanised antibodies (see AAY22262 and AAY32265), which comprise sufficient of the amino acid sequences of the Cll light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble cops formation in human therapy, for the treatment of arthritis, cops formation in human therapy, for the treatment of arthritis, classes, viscitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Solgren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cromn's disease, Solgren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cromn's disease, Copi, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignanches (claimed). They are also useful convenient and various ligands and acceptance of the property of the principal particularly changes and particularly are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable domain; lambda light chain; Catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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                                                                                                                                                                                                                                                                                                                                             Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                             Ellis JH, Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain CDR2 of catalytic antibody 389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining the binding agents.
                       /note= "CDR L2"
125..134
                                                                         "CDR L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 2; 81pp; English.
                                                                                                                                                                                                           99WO-GB01434.
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                                                                                                                                                                                                                                                                                                                                             Crowe SJ,
                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-053101/04.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ34746
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AAW39816;

RESULT 13 AAW39816

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Length 7; ó; Indels

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Search completed: April 22, 2003, 12:51:12 Job time : 18.75 secs
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                                                                                                                                                                                           AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transitions state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl occaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "complementarity determining region 2 of the
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                                                                     New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /notes "complementarity determining region 1 of 119ht chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%; Score 28; DB 19; Length 113; llarity 85.7%; Pred. No. 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single chain Fv region of the catalytic antibody 3B9.
                                                                                                                                                              Claim 12; Pages 71-72; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW39899 standard; Protein; 274 AA.
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               WPI; 1998-077166/07.
P-PSDB; AAV09791.
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Best Local Similarity
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55 LMSTRSS
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The present sequence represents the single chain FV region of the monoclonal catalytic antibody 3B9, which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAB) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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85.7%; Pred. No. 91;
iive 1; Mismatches 0; Indels
                           259..263 _
/note= "Flag epitope sequence"
light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 27; 147pp; English.
                                                                                                                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                      96US-0672345.
                                                                                                                                                                                                                               97WO-US10965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-077166/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        simply binding
                                                                                                                                                                                                                               25-JUN-1997;
                                                                                                                                                                                                                                                                                   25-JUN-1996;
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                                                                                                                                                                        31-DEC-1997.
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Matches 7; Conservative
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US-09-840-459-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        April 22, 2003, 12:53:59 ; Search time 7.375 Seconds (without alignments) 76.055 Million cell updates/sec
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1. /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4. /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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                                GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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10 US-09-864-761-33844

10 US-09-955-301-884

9 US-09-712-363-281

10 US-09-66-159

10 US-09-64-761-45487

10 US-09-764-877-1708

9 US-10-085-37-784

9 US-09-866-050A-336

9 US-09-866-050A-316

9 US-09-862-936A-31

9 US-09-829-936A-31

9 US-09-829-936A-31

9 US-09-829-936A-31

9 US-09-829-936A-31

9 US-09-9329-308-691

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301932 seqs, 80129803 residues
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Listing first 45 summaries
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20 22 774 443 9 US-0-1015746-318 Sequence 318, App 22 2 4 774 443 9 US-0-1015746-318 Sequence 318, App 22 2 4 774 443 9 US-0-1015-218-318 Sequence 318, App 22 2 4 774 443 9 US-0-1015-218-318 Sequence 318, App 22 2 4 774 443 9 US-0-1016-218-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-218-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-147-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-147-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-147-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-147-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-147-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1016-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 32 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-22-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774 443 9 US-0-1012-32-318 Sequence 318, App 42 2 4 774
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us-09-674-716b-5.open.rapb

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US-09-712-363-281

Sequence 281, Application US/09712363

Patent No. US2020164588A1

Sequence 281, Application US/09712363

Patent No. US2020164588A1

APPLICANT: Eleenberg, David

APPLICANT: Marcotte, Edward M.

ITILE OF INVENTION: DETERMING THE FUNCTIONS AND

ITILE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

ITILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT APPLICATION NUMBER: 06/179,531

PRIOR FILING DATE: 2000-01-01

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01

PRIOR PELING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/114,093

PRIOR PELING DATE: 1999-02-01

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-05-14

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12
     Gaps
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US-09-251-301-884
| Sequence 884, Application US/09925301
| Sequence 884, Application US/09925301
| Patent No. US200200523081
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO NUMBER: US/09/925,301
| CURRENT FILING DATE: 2001-08-10
| PRIOR PILING DATE: 2001-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1694
| SOFTWARE PATENT NOS: 1694
| SEQ ID NO 884
| LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 83.9%; Score 26; DB 10; Length 449; Best Local Similarity 85.7%; Pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 1; Indels
2; Mismatches
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-884
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62 MMTTRAS 68
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Matches
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                                                FEATURE:

OTHER INFORMATION: MAP TO ACOO7786.1

OTHER INFORMATION: EXPRESSED IN HBLIOO, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HRATY, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BRATY, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PELACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
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Pred. No. 42;
                    Sequence 33844, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Loce Similarity
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1708
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Sequence 1708, Application US/09764877

Sequence 1708, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT APPLICATION UNBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 1708

TENGTON 1708
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45
OTHER INFORMATION: EST_HUMAN HIT: AU121127.1, EVALUE 1.50e-02
US-09-864-761-45497
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77.4%; Score 24; DB 10; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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77.4%; Score 24; DB 10; Length 32;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels
         PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00668
PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: US 00/234,687
PRIOR PELICATION NUMBER: US 00/234,687
PRIOR PELICATION NUMBER: US 00/774,203
PRIOR PELICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PELICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 45487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (107)
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# APPLICANT: Rank, David R.
# APPLICANT: Chen, Wensheng
# TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
# TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
# TITLE OF INVENTION: HUMBER: US/09/864,761
# CURRENT PAPLICATION NUMBER: US 60/180,312
# PRIOR PAPLICATION NUMBER: US 60/180,312
# PRIOR PAPLICATION NUMBER: US 60/207,456
# PRIOR PAPLICATION NUMBER: US 60/207,456
# PRIOR PAPLICATION NUMBER: US 60/236,356
# PRIOR PAPLICATION NUMBER: US 60/236,356
# PRIOR PAPLICATION NUMBER: US 60/236,356
# PRIOR PAPLICATION NUMBER: US 60/236,359
# PRIOR PAPLICATION NUMBER: PCT/US01/00666
# PRIOR PAPLICATION NUMBER: PCT/US01/00666
# PRIOR PILING DATE: 2000-10-30
# PRIOR PILING DATE: 2001-01-30
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US-10-60-036-159
i Sequence 159, Application US/10060036
j Publication No. US20030073144A1
i GENERAL INFORMATION:
i APPLICANT: Benson, Darin R.
i APPLICANT: Realos, Michael D.
i APPLICANT: Lodes, Michael J.
i APPLICANT: Hepler, William T.
i APPLICANT: Hepler, William T.
i APPLICANT: However, William T.
i APPLICANT: However, William T.
i TITLE OF INVENTION: COMPOSITIONS AND MEGHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 210121.566
i CURRENT FILING DATE: 2002-01-30
i NUMBER OF SEQ ID NOS: 4560
i SOFTWARE: FORESEQ FOR WINDOWS VERBION 4.0
i SEQ ID NO 159
i LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 83.9%; Score 26; DB 9; Length 1464; Local Similarity 85.7%; Pred. No. 6e+02; les 6; Conservative 0; Mismatches 1; Indels
                                                                                                               Query Match
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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Patent No. US20020048763A1
i TYPE: PRT
i ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-036-159
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US-09-864-761-45487
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RESULT 11
US-09-829-936A-31
US-09-829-936A-31
Squence 31, Application US/09829936A
Publication No. US20030049699A1
GENERAL INFORMATION:
TITLE OF INVENTION: P63 Protein
TITLE OF INVENTION: P53 Protein
TITLE REFERENCE: ST98033
TITLE REFERENCE: ST98033
FILE REFERENCE: ST98033
CURRENT APPLICATION NUMBER: US/09/829,936A
CURRENT PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: F89812754
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
LENGTH: 298
LENGTH: 295
LENGTH: 295
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CURRENT PAPLICATION NUMBER: US/10/005,057A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/251,555
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Post Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
PRATURE:
CONTEX INFORMATION: Fragment C-term MBP1 murine
US-09-829-936A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Human fragment C-term MBP1
US-09-829-936A-31
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Patent No. US20020170097A1
SERERAL INFORMATION:
APPLICANT: Tao, Yumin
APPLICANT: Gordon-Karm, William J.
APPLICANT: Shen, Bo
APPLICANT: Lowe, Keith S.
APPLICANT: Danilevskaya, Olga
APPLICANT: Mahajan, Pramod
APPLICANT: Mahajan, Pramod
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Klein, Ted M.
PRIOR APPLICATION NUMBER: FR9812754
PRIOR FILING DATE: 1998-10-12
NUMBER OF SEQ ID NOS: 33
SSOFWARE: Patentin version 3.1
SSO ID NO 9
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 85./v
Best Local 6; Conservative
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Publication No. US20030049699A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharma, S.A.
TITLE OF INVENTION: P61yopeptide (MBP1) Capable Of Interacting With Oncogenic Mutante
FILE REFERENCE: ST98033
CORRENT APPLICATION NUMBER: US/09/829,936A
CURRENT FILING DATE: 2001-04-11
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US-09-866-050A-336

is-09-866-050A-336

is Sequence 336, Application US/09866050A

is Publication No. US20030040471A1

is GENERAL INFORMATION:

is APPLICANT: Strachan, Lorna

is APPLICANT: Strachan, Lorna

is APPLICANT: Steaman, Matthew

is APPLICANT: Steaman, Matthew

is APPLICANT: Kumble, Krishanand

is APPLICANT: Kumble, Krishanand

is TITLE OF INVENTION: Compositions Isolated From Skin Cells

if TITLE OF INVENTION: Compositions for Their Use

if TITLE OF INVENTION: and Methods for Their Use

if TITLE OF INVENTION: UNMERR: US/09/866,050A

is CURRENT FILING DATE: 2201-05-24

is SOFTWARE: FastSEQ for Windows Version 4.0

is ENNETH: STATES OF THE US OF THE US OF US 
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                                                                                          RESULT 8

WS-10-083-357-784

Sequence 784, Application US/10083357

Publication No. US20030054370A1

GENERAL INFORMATION:

APPLICAMT Glandong Zeng et al.

TITLE OF INVENTION: Systemic Discovery of New Genes

FILE REFRENCE: 032796-090

CURRENT PELING DATE: 2002-02-27

NUMBER OF SEQ ID NOS: 1346

SEQ ID NO 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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19 LMTTRGS 25
          67 LPSTRAS 73
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; ORGANISM: Human
US-09-866-050A-336
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US-09-829-936A-9
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Sequence 78, Application US/09908711

Sequence 78, Application US/09908711

SENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL28

CURRENT APPLICATION NUMBER: US/09/908,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 305;
                                                                                                                                                                                                                                                                                                         Query Match
77.4%; Score 24; DB 9; Length 297;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Misma@ches 0; Indels
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77.4%; Score 24; DB 9; Length 30:
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-738-626-4088

US-09-738-626-4088

Sequence 4008, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: NAKOGUCHI, HIROSHI
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCKIAI, KEIKO
APPLICANT: YOKOI, HARVEHIKO
APPLICANT: YOKOI, HARVEHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PAEINTIN VET: 3.0
SEQ ID NO 4088
LENGTH: 305
TURNE: PAINT
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 297
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                              ; NAME/KEY: VARIANT
; LOCATION: (1)...(425)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-005-057A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4088
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246 VMSSRAS 252
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66 LLSTRA 71
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CURRENT FILING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR
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NUMBER OF SEQ ID NOS: 167

SOUTHER: Parter.

SOUTHER: Parter.

NOS: 167

SOUTHER: NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

SOUTHER: NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

SOUTHER: NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NOS: 167

OCHER INFORMATION: NOS: 167

SOUTHER PARTER.

SOUTHER PARTER.

SOUTHER PARTER.

SOUTHER: 199-03-12

SOUTHER: 199-03-12

SOUTHER: PARTER.

SOUTHER: PARTER.

SOUTHER: NOS: 199-03-12

SOUTHER: PARTER.

SOUTHER: 199-03-12

SOUTHER: PARTER.

SOUTHER: PART
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Search completed: April 22, 2003, 13:11:12 Job time : 8.375 secs

||| ||| 413 LMSYRAS 419

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 12:48:24; Search time 8.83929 Seconds (without alignments) 97.882 Million cell updates/sec Run on:

US-09-674-716B-7 Title: Perfect score:

1 QQLVEYPFT 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results fredicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ubiquinol-cytochro	Ig kappa chain V r	kappa	Ig kappa chain V r		probable calmoduli	Ig lambda chain V	sphati	Ig kappa chain pre	hypothetical prote					•–	Ig kappa chain V r	lysozyme (EC 3.2.1	hypothetical prote	glycerol-3-phospha	ubiquinol-cytochro	B. subtilis YxiO p	. subtilis Yxio	3',5'-cyclic-nucle	long-chain-fatty-a	long-chain-fatty-a	long-chain-fatty-a		glycine-tRNA ligas	
SUMMARIES	ΙD	C42622	G30538	KVMS16	KVMS51	KVMS67	A85363	836277	T38148	B29775	A86371	D82100	D89903	876367	T01906	126317	D26317	AD3322	D83163	D90527	S41834	AG1614	A11251	A25346	S41589	B90943	F85791	AC0725	F70483	T21138
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de	Query	89.6	87.5		87.5	77.1	77.1	75.0	75.0	72.9	72.9	70.8				68.8		68.8	68.8	68.8	68.89	68.8	68.8	æ	8	æ	68.8	e.	68.8	68.8
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	Result No.	1	7	e	4	D.	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig Rappa chain V region (253.15E2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus graduence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30538
R;Claflin, J.L.; Berry, J.

:||:||||| 341 KQLIEYPFT 349 1 QQLVEYPFT 9

ò g RESULT 2 G30538

	ig light chain v r Ig kappa chain pre Ig kappa chain - h unknown protein, 7	hypothetical prote probable 2-hydroxy probable dicarboxy biliverdin reducta	biliverdin reducta biliverdin reducta hypothetical prote conserved hypothet	probable bulk DNA-
846268 T15138 165317	B49060 A29775 S40334 G96705	AF2397 T45421 T49628 A42268	G02066 S62624 T01948 F69999	A85019
010141	2000	0000	2222	10
816 817 61	112 120 132 151	180 242 282 295	296 296 398	315
68.8 68.8 66.7	66.7 66.7 66.7 66.7	66.7 66.7 66.7 66.7	66.7	66.7
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30 32 32	ህ ህ ህ ህ ህ ላ ህ ህ	37 39 40	4 4 4 4 1 2 6 4	. 4. ?

ALIGNMENTS

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ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - honeybee mitochondrion C;Species: mitochondrion Apis mellifera (honeybee)
A;Variev: liguestica
C;Variev: liguestica
C;Accession: C42622; S52971
R;Crozier; R.H.; Crozier; Y.C.
Wol. Biol. Bvol. 9, 474-482, 1992
A;Title: The cytochrome b and ATPase genes of honeybee mitochondrial DNA.
A;Reference number: A42622; MUID:92261310; PMID:1533894
A;Reference number: A42622; MUID:92261310; PMID:1533894
A;Reference number: A72622; MUID:92261310; PMID:1533894
A;Residues: 1-383 - CRO.
A;Residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: mitochondrion
A; Genome: code: SGC4
C; Superfamily: cytochrome b, cytochrome b homology; oytochrome b6 homology; plastoquinol.
C; Superfamily: cytochrome b; cytochrome transfer; heme; iron; metalloprotein; mitochondrion,...
F;14-340/Domain: cytochrome b homology cCBH>
F;14-211/Domain: cytochrome b6 homology cCBH>
F;223-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology c17K>
F;85,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted F;99,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
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A;Moleovile type: DNA
A;Residues: 1-383 <CR2>
A;Cross-references: EMBL:L06178; NID:g336279; PIDN:AAB96809.1; PID:g552449
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89.6%; Score 43; DB 2; Length 383;
Best Local Similarity 77.8%; Pred. No. 0.55;
Matches 7; Conservative 2; Mismatches 0; Indels
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A) Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfidab bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IWM>

F;43-115/Domain: immunoglobulin homology <IWM>
                                                                                                                                                                                                                                                                                                                                                         Tile kappa chain precursor V region (VK167) - mouse cipateles; Mus musculus (house mouse) Cipateles; Mus E. Storb, U.

Risclaing, E.; Storb, U.

A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes. A;Reference number: A01909; MUID:82002223; PMID:6791832 A;Accession: A01909
A;Accession: A01909
A;Accession: A01909
A;Notecule type: DNA
A;Residues: 1-120 <&RL>
A;Note: the sequence was determined from the germline gene C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig lambda chain V region (clone alpha-FOGI-G8) - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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2.8;
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Similarity 75.0%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A, Map position: 4
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836277
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accesion: A01910
R;Appella, E.
Mol. Immunol. 17, 711-718, 1980
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcho
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcho
A;Accession: A01910
A;Accession: A01910
A;Residues: 1-113, -APP
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Complex: An immunoglobulin heterotecraemer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into Ia
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IVMN
F;23-93/Domain: immunoglobulin predicted
F;23-93/Domain: immunoglobulin predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipecies: Musculus (house mouse)
Cipecies: Musculus (house mouse)
Cipate: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
Cipate: 30-Nov-1980 # Corter, No. 1998
Rivalivoff: S.; Potter, No. 1978
Rivalivoff: No
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Accession: G30538
A;Accession: G30538
A;Accession: G30538
A;Cession: G30538
A;Cession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.5%; Score 42; DB 1; Length 112; Best Local Similarity 88.9%; Pred. No. 0.24; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5%; Score 42; DB 2; Length 74; Best Local Similarity 88.9%; Pred. No. 0.16; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 QQLVEYPLT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 QQLVEYPLT 71
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F;36-115/Domain: immunoglobulin homology <IMM>
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114 QQIVEYP 120
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                                                                                                                                                                       1 QQLVEYP 7
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           C; Accession: S36277

K; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993

A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S3625; MUID:93178448; PMID:7679990

A; Reference number: S3625; MUID:93178448; PMID:779990

A; Status: preliminary; nucleic acid sequence not shown
A; Status: preliminary; nucleic acid sequence not shown
A; Status: mRNA
A; Residues: 1-108 < GRI>
A; Cross-references: EMBL:218829; NID:933417; PIDN:CAA79281.1; PID:9939910
C; Superfamily: immunoglobulin immunoglobulin homology
C; Keywords: heteroctetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiAccession: T38148

Riperation. D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

Riperation. D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

A; Reference number: Z21774

A; Reference number: Z21774

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Molecule type: DNA

A; Cross-references: EMBL: Z99295; PIDN: CAB16578.1; GSPDB:GN00066; SPDB:SPAC22A12.08c

A; Experimental source: strain 972h-; cosmid c22A12
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: B29775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Schizosaccharomyces pombe
.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R;Jouvin-Marche, E.; Rudikoff, S.

Immunogenetics 24, 191-201, 1986

A;Title: Evolution of a V-kappa gene family.

A;Reference number: A91751; MUID:87006895; PMID:3093373

A;Mocession: B29775

A;Molecule type: DNA

A;Residues: 1-120 < dJU>

A;Cross-references: GB:MIS553; NID:g197470; PIDN:AAA39037.1; PID:g197471

A;Note: this sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Ajutrons: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
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75.0%; Score 36; DB 2; Length 570;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 36; DB 2; Length 108;
66.7%; Pred. No. 4;
iive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C'Genetics:
A;Gene: SPDB:SPAC22A12.08c
A;Map Dosfition: 1
A;Introns: 43/2; 62/2; 227/2; 483/1
                                                                                                                                                                                                                                                                                                                                                                                     :||||| ||
547 KQLVEYSFT 555
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89 QQLISYPLT 97
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T38148
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mesJ protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Accession: D82100
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
R;Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, Pl.
R; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Heference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82100
A;Astatus: preliminary
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Dacession: A86371
C;Accession: A86371
C;Accession: A86371
C;Accession: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Theologis, A.; Ecker, J.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.W.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Athle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Status: preliminary
A;Nolecule type: DNA
A;Reidues: 1-480 <STO>
A;Reidues: 1-480 <STO>
A;Coss-references: GB:AE005172; NID:g4056452; PIDN:AAC98025.1; GSPDB:GN00141
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Length 120;
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Score 35; DB 2;
Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2; Pred. No. 31; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.8%; Score 34; DB
llarity 75.0%; Pred. No. 46;
Conservative 0; Mismatches
                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%;
85.7%;
   th 72.9%; Similarity 85.7%; 6; Conservative
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Matches 6; Conserv
      Query Match
Best Local Similarity
Matches 6; Conserv
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Gaps

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Gypecies: Mus musculus (H158-89H4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: 126317
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MuID:86300658; PMID:2427335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Wolecule type: DNA
A; Residuee: 1-12 < CAT-
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C; Superfamily: immunoglobulin vi region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.8%; Score 34; DB 2; Length 1074; Best Local Similarity 71.4%; Pred. No. 1.2e+02; Matches 5; Conservative 2; Mismatches 0; Indels
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A; Description: The sequence of A. thaliana T12H20.
A;Reference number: 214453
A;Recession: T01906
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-1074 <COT>
A;Cross-references: EMBL;RF080119; NID:g3600029; PID:g3600033
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Note: T12H20.3
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95 QHLEYPFT 102
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853 ELIEYPF 859
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A; Accession: S76367
A; Accession: S76367
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-722 < KAN>
A; Cross-references: BMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10219.1; PID:g100159
A; Cross-references: BMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10219.1; PID:g100159
C; Superfamily: glycine-tRNA ligase beta chain
                                                                                                                                                                                                                                                                       hypothetical protein SA1131 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: D89903
S;Accession: D89903
S;Aucession: D89903
S;A
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Lypothetical protein - Synechocystis sp.
Lypothetical protein - Synechocystis sp.
Lybariety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Datession: S76367
C;Accession: S76367
C;Accession: S76367
C;Accession: S76367
C; Ataneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res: 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SA1131
C;Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-treferences: GB:BA000018; PID:g13701089; PIDN:BAB42384.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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85.7%; Pred. No. 78;
ative 1; Mismatches 0; Indels
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Best Local Similarity 85.77
**** 6; Conservative
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109 QLIELPFT 116
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T01906
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EWBL; L06178; AAB96809.1; -.
EWBL; M87052; -; NOT_ANNOTATED_CDS.
EMBL; (42622; C42622; InterPro; IPR00179; Cyt. b b6.
Ffam; PF00032; Cytochrome_D_C; 1.
Ffam; PF00033; Cytochrome_D_C; 1.
FROSITE; PS00192; CYTOCHROME_B HENB; 1.
FROSITE; PS00193; CYTOCHROME_B GO; 1.
                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Cytochrome B.
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CYB APILI
ID CYB APILI
AC P34845;
mus musculu
akodon jels
akodon torq
sigmodon hi
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rattus norv
homo sapien
borrelia bu
bolomys amo
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mus musculu
mus musculu
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pasteurella
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cervus nipp
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dama dama (
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escherichia
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mus musculu
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bacillus li
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arctocephal
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                                                                                                                April 22, 2003, 12:46:53; Search time 4.5 Seconds (without alignments) 82.953 Million cell updates/sec
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P01626
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P25269
               GenCore version 5.1.4 ps 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                 112892 segs, 41476328 residues
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CN17_D1CD1
LCFA_ECOL1
SYGE_AQUAE
ATX1_MOUSE
ATX1_HUMAN
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YOO BORBU

YOO BORBU

CYB BOLAM

CYB BOLAM

MSRB BOLAM

MSRB CYACA

TYSY METVA

TYSY METVA

HNLS SORBI

CYB ALCA

TYSY METVA

HNLS SORBI

CYB ALCA

CYB ARBCT

CYB ARCCG

CYB ARBCT

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KV2Ā MOUSĒ
KV2C MOUSĒ
KV2E MOUSĒ
CYB ĀKOJĒ
CYB ĀKOJĒ
CYB SIGHI
SYGĒ SYNY3
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Sequence:
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                                                                                   OM protein
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09tf32 eutamias do 048372 glaucomys s 047930 hydropotes 03593 saimiri sci 03589 sciurus nig 09tf51 spermophilu P4041 spermophilu P4041 spermophilu P60156 homo sapien 03372 microtus ar P56731 microtus ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- FUNCTION: COMPURENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
--- COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAINT THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED IO ATP SYNTHESIS.
--- COFACTOR: TWO HEME GROUDS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Apoidea; Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crozier R.H., Crozier Y.C.; "The cytochrome b and ATPase genes of honeybee mitochondrial DNA."; Mol. Biol. Evol. 9:474-482(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crozier R.H., Crozier Y.C.,
"The mitochondrial genome of the honeybee Apis mellifera: complete
sequence and genome organization.";
Genetics 133:97-117 (1993).
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apis mellifera ligustica (Common honeybee). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                             CYB_HYDIN
CYB_SAISC
CYB_SCINI
CYB_SPEAN
CYB_SPEAN
CYB_SPERI
CYB_HUMAN
CYB_HUMAN
CYB_HUMAN
CYB_HICLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Thorax;
MEDLINE=93114603; PubMed=8417993;
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MEDLINE=92261310; PubMed=1533894;
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Best Loca Matches

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RX Appella E.;
RT Appella E.;
RT Phosphory-tholine-binding mutine myeloma protein.";
RT Phosphory-tholine-binding mutine myeloma protein.";
RT Phosphory-tholine-binding mutine myeloma protein.";
RL MOL. Immunol. 17:714-718(1980).
CC BINDS PHOSEPHORY-CHOLINE.
DR PRESP PROSECTIONS.
CC BINDS PHOSEPHORY-CHOLINE.
DR PRESP PROSECTIONS.
DR RESP PROSECTIONS.
DR REAM, PROOSESTION.
DR REAM, PROOSESTION.
DR SWART, SMO0406; IGV.
DR REAMS.
DOWAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
FT DOWAIN 40 54 COMPLEMENTARITY-DETERMINING-2.
FT DOWAIN 52 93 FRAMEWORK-3.
FT DOWAIN 103 112 FRAMEWORK-3.
FT DOWAIN 103 112 FRAMEWORK-4.
FT DOWAIN 103 112 FRAMEWORK-4.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBL_TaxID=10090;
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Selaing E., Storb U.;
"Somatic mutation of immunoglobulin light-chain variable-region
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Local Similarity 88.9%; Pred. No. 0.15;
se 8; Conservative 0; Mismatches 1; Indels
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12496 MW; EFB0DC4DA2BD3450 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-II region VKAPPA167 precursor.
Mus musculus (Mouse)
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                                                                                                                                               [1]
SRQUENCE.
MEDLINE=81052016; Pubmed=6776396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, J00562; AAA39032.1; -. EMBL; K02415; AAA39051.1; -. PIR; A01909; KVWS67. HSSP; P80362; IWTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Čell 25:47-58(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 QQLVEYPLT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               Gaps
           Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. Ol, Created)
21-JUL-1986 (Rel. Ol, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region MOPC 167.
Mus musculus (Mouse).
Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                     95 IRON 1 (HEME B562 AXIAL LIGAND).
99 IRON 2 (HEME B566 AXIAL LIGAND).
184 IRON 2 (HEME B562 AXIAL LIGAND).
198 IRON 1 (HEME B566 AXIAL LIGAND).
45256 MW, A140A05E6053C2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
PRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                                                                                                                      / Match
89.6%; Score 43; DB 1; Length 383;
Local Similarity 77.8%; Pred. No. 0.32;
les 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5%; Score 42; DB 1; Length 112; 88.9%; Pred. No. 0.15; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12349 MW; A58EDFD6404B9726 CRC64;
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(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig, 1.
SWART; SM00466; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 88.9%;
es 8; Conservative
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99
184
198
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39
54
61
102
112
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184
198
383 AA;
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                                                                                                                                                                                                                                                                                                                                                                   341 KQLIEYPFT 349
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21-JUL-1986
15-JUL-1999
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P01628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV2A MOUSE
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NON TER
SEQUENCE
                                                                                                                                               METAL
SEQUENCE
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(V2A_MOUSE

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AC FOLD 56

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DE 9016 56

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KV2C_MOUSE
ID KV2C_M
AC P01628
AC P1 21-JUL
DT 21-JUL
DT 15-JUL
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DOMAIN

Best Loc Matches

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RESULT 6
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XX MEDLINE=9163325; PubMed=2002767;
XX MEDLINE=91163325; PubMed=2002767;
XX MEDLINE=91163325; PubMed=2002767;
XX Smith M.F., Patton J.L.;
YX Sigmodontinae).",
XX Sigmodontinae).",
XX Sigmodontinae).",
XX MALAT SUBJUINOL-CYTOCHROME C REDUCTASE
XX TOWPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
XX STREPFFATORY THAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
XX COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX)
XX COMPLEX TWO HEME GROUPS (8562 AND 8566) WHICH ARE NOT COVALENTLY
XX SUBJUINT: THE MAIN SUBJUINS OF COMPLEX B-C1 ARE: CYTOCHROME B,
XX CYTOCHROME C1 AND THE RIESKE PROTEIN.
XX SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
                                                                                                                                                                                                ö
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                               IG KAPPA CHAIN V-II REGION VKAPPA167. FRAMEWORK-1.
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0
                                                                                 COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                               COMPLEMENTARITY-DETERMINING-3. BY SIMILARITY.
                                                                                                            COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                          DB 1; Length 120;
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith M.F.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 0; Indels
                                                                                                                                                      63BB571F0E4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                  379 AA
                                                                                                                                                                          77.1%; Score 37; DB 100.0%; Pred. No. 1.6; ive 0; Mismatches
                                                                                                                       FRAMEWORK-3
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; l.
SMART; SM00406; IGv; l.
Immunoglobulin V region; Signal.
                                                                                                                                                        13280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-133 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-267 FROM N.A.
                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                  Cytochrome B.
MTCYB OR COB OR CYTB.
Akodon jelskii.
                                                                                                                                                        120 AA;
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10079;
                                                                                                                                                                                                                                            114 QQLVEYP 120
                                                                                                                                                                                                                        1 QQLVEYP 7
                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissue=Liver;
                                                                                                                                                                                                                                                                                                 CYB AKOJE
P21715;
                                                                                                                                            DISULFID
                                                                              DOMAIN
                                                                                                   DOMAIN
                                                         SIGNAL
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                              RESULT 5
CYB_AKOJE
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=MVZ catalog 171720, 171721, 174053, and 174054; TISSUE-Liver;
STRAIN=MVZ catalog 171720, 171721, 174053, and 174054; TISSUE-Liver;
MEDIATE-91163325; PubMed=2002767;
Smith M.F., Patton J.L.;
"Variation in mitochondrial cytochrome b sequence in natural
populations of South American akodontine rodents (Muridae:
Signaciontinae).";
Mol. Biol. Bvol. 8:85-103(1991).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                EMBL; M35114; AAA16998.2; ALT_TERM.
EMBL; M35715; AAA31629.1; -.
EMBL; M35715; AAA31629.1; -.
EMBL; (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (41824); (4
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"The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
Biol. J. Linn. Soc. Lond. 50:149-177(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 IRON 1 (HEWE B562 AXIAL LIGAND).
97 IRON 2 (HEME B566 AXIAL LIGAND).
182 IRON 2 (HEWE B562 AXIAL LIGAND).
196 IRON 1 (HEME B566 AXIAL LIGAND).
118 V -> I (IN STRAINS 173083 AND 173084).
122 T -> A (IN STRAINS 173083 AND 173084).
42559 MW; F9F012A46671D59A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith M.F.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-267 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome B. MICYB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Local 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
379 AA;
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 OPVEYPFT 348
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUPLED TO ATP SYNTHESIS.
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
-!- SUBGNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIBSKE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                        EMBL, M35700; AAA18897.2; -.
EMBL, M35701; AAA31624.1; -.
EMBL, M35702; AAA31625.1; -.
EMBL, M35702; AAA31625.1; -.
EMBL, M35702; AAA31625.1; -.
EMBL, M35702; CAPCONTON E.
EMBL, M35702; CAPCONTON E.
EMBL, M35702; CAPCONTON E.
EMBL, M35702; CAPCONTROME E.
EMBL, M35702; CAPCONTROME E.
EMBL, M35703; CYTOCHROME E.
EMBL, M35703; CYTOCHROME E.
ELECTRON transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 IRON 1 (HEME B562 AXIAL LIGAND).
97 IRON 2 (HEME B566 AXIAL LIGAND).
182 IRON 1 (HEME B562 AXIAL LIGAND).
196 V -> A (IN STRAINS 174053 AND 174054).
115 V -> I (IN STRAINS 174053 AND 174054).
42611 MW; 4C94CPBA92CCC34F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOUND TO THE PROTEIN.
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome B.
MTCYB OR COB OR CYTB.
Sigmodon hispidus (Hispid cotton rat).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 87.5
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97
182
196
108
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379 AA;
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Q9XNU6;
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SEQUENCE
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CYB SIGHS

O 95NN

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DT 15-J
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055690;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
01-NOY-1-ENNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase dLYS OR SLR0220.
                                                                                                                                                                                                        EMBL, AF108702, AAD45484.1; -.
InterPro; IPR000379; Cyt b b6.
Pfam; PF00032; cytochrome D C; 1.
Pfam; PF00033; cytochrome D N; 1.
PROSITE; PS00193; CYTOCHROME B. HEME; 1.
PROSITE; PS00193; CYTOCHROME B. GO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
0472259421B38284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 36; DB 1; Length 381; 87.5%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + glycyl-trna(gly).
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis.
Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002311; tRNA synt_2f.
Pfam; PF02092; tRNA synt_2f; 1.
PRINTS; PR01045; TRNASYNTHGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 83 IRC
97 97 IRC
182 182 IRC
196 IRC
381 AA, 42965 MW, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 87.5
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-!- SIMILARITY: BELONGS TO THE CAMP PHOSPHODIESTERASE CLASS-II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-69 FROM N.A.

MEDLINE=87010528; PubMed=3020155;
Podgorski G.J., Franke J., Kessin R.H.;
Podgorski G.J., Franke J., Kessin R.H.;
Podgorski G.J., Pranke J., Kessin R.H.;
Podgorski G.J., Pranke J., Kessin R.H.;
Prodgoling a portion of the cyclic nucleotide
phosphodiesterase of Dictyostellium discoideum.";
J. Gen. Microbiol. 132:1043-1050(1986).
-i. FUNCTION: TO MAINTAIN THE RESPONSIVENESS OF CELLS TO THE
CHEMOATTRACTANT CAMP DURING THE AGGREGATION PHASE OF DEVELOPMENT.
TIGRFAMS; TIGR00211; glyS; 1.
PROSITE; PS50861; AA TRNA LIGASE II GLYAB; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3',5'-cyclic-nuclectide phosphodiesterase precursor (EC 3.1.4.17)
(PDEase) (3':5'-CNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lacombe M.-L., Podgorski G.J., Franke J., Kessin R.H.; "Molecular cloning and developmental expression of the cyclic nucleotide phosphodiesterase gene of Dictyostelium discoideum."; J. Biol. Chem. 261:16811-16817(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINES #9384621; PubMed=2779573;
MEDLINES #9384622; PubMed=2779573;
Podgorski G.J., Franke J., Faure M., Kessin R.H.;
Prde cyclic nucleotide phosphodiesterase gene of Dictyostelium
"The cyclic nucleotide phosphodiesterase gene of Dictyostelium
discoideum utilizes alternate promoters and splicing for the
sinchesis of multiple mRNAs.";
Mol. Cell. Biol. 9:1938-3950(1989).
                                                                                                                                                                                                                                                                               ö
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Similarity 85.7%; Pred. No. 38;
6; Conservative 1; Mismatches 0; Indels
                                                                                                                                     722 AA; 80051 MW; F7085BA5A23436D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold),
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 AA
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InterPro; PR000396; Pddesterase2.
Pfam; PF02112; PDEase II; 1.
PRINTS; PR00388; PDIESTERASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87057386; PubMed=3023365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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PIR; A32573; A32573.
                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                            Complete proteome
SEQUENCE 722 AA
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254 EQLVEYP 260
                                                                                                                                                                                                                                                                                                                                                    1 QQLVEYP 7
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01-FEB-1996
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Black P.N., Dirusso C.C., Metzger A.K., Heimert T.L.; electrichia "Cloning, sequencing, and expression of the fadb gene of Bscherichia ecoli encoding acyl coenzyme A synthetase."; cli encoding acyl coenzyme A synthetase."; J. Biol. Chem. 267:25513-25520(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fulda M., Heinz E., Wolter F.P.;
"The fadD gene of Escherichia coli K12 is located close to rnd at 39.6 min of the chromosomal map and is a new member of the AMP-binding protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
MEDLINE=97251358; PubMed=9097040;
MEDLINE=97251358; PubMed=9097040;
ISONO K., Rasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Mocromura K.,
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampel G., Seki Y., Sivaeundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                     3',5'-CYCLIC-NUCLEOTIDE
PHOSPHODIESTERASE.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
NW -> LT (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
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                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1; Length 452;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                               A8F3C190D4603BD1 CRC64;
ProDom, PD010003; Pdiesterase2; 2.
PROSITE; PS00607; PDEASE II; 1.
Glycoprotein; Hydrolase; CAMP; Zinc; Signal.
Glycoprotein; 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 242:241-249(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
MEDLINE=93094273; PubMed=1460045;
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                                                                                                                                                                                                                                                                                       69 N
51093 MW;
                                                                                                                                                                                                                                                                                                                                                                           68.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                    452
                                                                                                                                                                                                    101
141
277
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FADD OR OLDD OR B1805.
                                                                                                                                                                                                                                                                                       68
452 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
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50
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P29212;
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CARBOHYD
CARBOHYD
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complete genome of the hyperthermophilic bacterium Aquifex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
SEQUENCE 664 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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248 LVEYPF 253
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P54254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
EcoGene; EG11530; rauu.
InterPro; IPR000873; AMP-bind.
Prostra: PR00501; AMP-binding; 1.
PROSITE; PS00455; AMP-BINDING; 1.
Ligase; Fatty acid metabolism; Magnesium; Membrane; Complete proteome.
CONFLICT 34 51 ARYADOPAFVNMGEVMTF -> GALRRSTCVCEYGGGNDI.
(IN REF. 2).
(IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40)
16-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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TRLKMSSCSMVAYRKSRLLAYLP (IN REF. A -> G (IN REF. 2).
GYVDNKA -> QSGQ (IN REF. 2).
249B0AA54B3DBFA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.8%; Score 33; DB 1; Length 561;
llarity 55.6%; Pred. No. 47;
Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X70994; CAA50321.1; -.
EMBL; L02649; AAA23752.1; -.
EMBL; BOR00275; AAC74875.1; -.
EMBL; D90823; BAA15600.1; -.
EMBL; D90824; BAA15609.1; -.
EMBL; D90825; BAA15614.1; -.
PIR; A45062; A45062.
HSSP; P08659; 1LCI.
ECGENE; EGI1530; fadD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62332 MW;
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555 5
561 AA;
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293 KELAKYPFT 301
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NCBI_TaxID=63363;
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067898;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6 X CBA; TISSUE=Brain, Thymus, and Retina;

XI MEDLINE=65381424 1 PubMed8487637;

Banfil S., Servadio A., Chung M.-Y., Capozzoli F., Duvick L.A.,

Elde R., Zoghbi H.Y., Orr H.T.;

Cloning and developmental expression analysis of the murine homolog

The spinocerebellar ataxia type 1 gene (Scal).";

C. -1 TISSUE SPECIFICITY: WIDELY EXPRESSED. IN BRAIN, THE PATTERN OF

DISTRIBUTION IS LIMITED TO NEURONS POPULATIONS.

C. -1 DEVELOPMENTAL STAGE: TRANSIENT EXPRESSION BURST IN PURKINJE CELLS

AS THE CEREBELLAR CORTEX BECOMES FUNCTIONAL (POSTNATAL DAY 14),

AND IN MESSENCHYMAL CELLS OF THE DEVELOPING INTERVERTEBRAL DISCS OF

THE SPINAL COLUMN:

C. -1 POLYMORPHISM: THE MURINE POLY-GLN REGION IS VERY LIMITED IN

C. -1 POLYMORPHISM: THE HUMAN SCAI AND IS NOT POLYMORPHIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                   + glycyl-trna(gly).
-!- SUBINIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
-(BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000775; AAC07870.1; -.
INTECPTO; IPR002311, TRNA synt_2f.
Pfam; PF02092; TRNA synt_2f, 1.
PRINTS; PR01045; TRNASNWTHGB.
TIGRAPMs; TIGR00211, gly5; 1.
PROSTER, PS50861; AA TRNA, LGASE II GLYAB; 1.
AMINOACY1-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%; Score 33; DB 1; Length 664; 100.0%; Pred. No. 56; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 AA; 77523 MW; 7FFEF7A8F552E3DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
30-MXY-2000 (Rel. 39, Last annotation update)
Ataxin-1 (Spinocerebellar ataxia type 1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     792 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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reductase)
                                                                                                                                                                                                                                                                 BIEA RAT
                                                                                                             Query Match
                                                                                                                                                                                                                                                                           P46844;
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                                                                                                                                       Matches
                                                                                                                                                                                                                                    RESULT 14
BIEA_RAT
                                                                                                                                                                                                                                                                           RESESES
SES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch)
                                                                                                                                                                  ö
 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE 1; ALSO KNOWN AS OLIVOPONTOCEREBELLAR ATROPHY I (OPCA I).
SCAI IS AN AUTOSOMAL DOMINANT NEUDODEGENERATIVED INSORDER
CHARACTERIZED BY PROCRESSIVE NEURONAL LOSS IN THE CEREBELLUM,
BRAIN STEM AND SPINOCEREBELLAR TRACTS. CLINICAL FEATURES ARE
CREBELLAR ATAXAL, DYSARTHAIA, OPHTALMOPARESIS, MISCLE MASTING AND
NEUROPATHY. ONSET OF THE DISEASE USUBLLY OCCURS IN THE THIRD OR
POURTH DECADE OF LIFE AND DEATH OCCURS TEN TO TWENTY YEARS LATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banfi S., Servadio A., Chung M.-Y., Kwiatkowski T.J. Jr., McCall A.E.,
Duvick L.A., Shen Y., Roth E.J., Orr H.T., Zoghbi H.Y.;
"Identification and characterization of the gene causing type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATUR SPLICING.
-!- TISSUB SPECIFICITY: MIDELY EXPRESSED THROUGHOUT THE BODY.
-!- POLYMORPHISM: THE POLY-GLN REGION OF SCA1 IS HIGHLY POLYMORPHIC (9 TO 39 REPRATS) IN THE NORMAL POPULATION AND IS EXPANDED TO ABOUT 40-81 REPEATS IN SCA1 PATIENTS. LONGER EXPANSIONS RESULT IN BARLIER ONSET AND MORE SEVERE CLINICAL MANIFESTATIONS OF THE DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: DEFECTS IN SCA1 ARE THE CAUSE OF SPINOCEREBELLAR ATAXIA
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE PRODUCED BY
                                                                                                                                     68.8%; Score 33; DB 1; Length 792; 100.0%; Pred. No. 66; 0; Mismatches 0; Indels
                                                                                                           792 AA; 84052 MW; CASF59C0013499DB CRC64;
                                                                                                                                                                                                                                                                                     ATXI HUMAN STANDARD; PRT; 816 AA. PS4553; O9UJG2; O1-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Ataxin-1 (Spinocerebellar ataxia type 1 protein). SCA1 OR ATXI. HUMAN).
entities requires a license agreement (so send an email to license@isb-sib.ch)
                                                                                             POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cerebellum, and Brain;
MEDLINE=95038838; PubMed=7951322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79204; CAA55793.1; -. EMBL; AL009031; CAA15622.1; -.
                                                     MGD; MGI:104783; Scal.
InterPro; IPR003652; Atax_HMG.
SMART; SM00536; AXH; 1.
DOMAIN 214 217 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spinocerebellar ataxia.";
Nat. Genet. 7:513-519(1994).
                            EMBL; X83542; CAA58533.1; -.
                                                                                                                        Query Match
Best Local Similarity 100...
Since 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:10548; SCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                            3 LVEYPF 8
                                                                                                           SEQUENCE
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T. Site-directed mutagenesis of cysteine residues in biliverdin
"Site-directed mutagenesis of cysteine residues in biliverdin
reductase. Roles in substrate and cofactor binding.";

Eur. J. Biochem. 222.597-603(1994).

-! FUNCTION: CONVERTS BILIVERDIN TO BILIRUBIN; DISPLAYS TWO DISTINCT
PH OPTIMA USING A DIFFERENT COPACTOR AT EACH PH: NADH AT THE LOWER
PH 6.7-6.9 RANGE AND NADH AT PH 8.5-8.7. NADPH, HOWEVER, IS THE
PROBABLE COPACTOR IN BIOLOGICAL SYSTEMS.

-!- CATALYTIC ACTIVITY: Bilirubin + NAD(P) (+) = biliverdin + NAD(P) H.

-!- PATHWAY: FINAL STRP IN HEME METABOLISM.

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- SUBUNITY: TO B.COLI YHHX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fakhrai H., Maines M.D.; "Expression and characterization of a cDNA for rat kidney biliverdin reductase. Exidence suggesting the liver and kidney enzymes are the same transcript product."; J. Biol. Chem. 267:4023-4029(1992).
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (BC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                              ö
                        InterPro; IPR003652; Atax_HMG.
SWART; SM00536; AXH; 1.
Polymorphism; Triplet repeat expansion; Alternative splicing.
DOMAIN 197 226 POIY-GLN.
                                                                                                                                                                                                                                       DB 1; Length 816;
68;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                               87051 MW; D49BA5DB423D0777 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 AA
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                       68.8%; Score 33; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M81681, AAA40830.1; -.
InterPro; IPR000683; GFO_IDH_MocA.
Pfam; PF01408; GFO_IDH_MocA; 1.
Oxdoreductase; NAD; NADP; Zinc.
PROPEP 3 295 BILIV.
CHAIN
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                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                   SEQUENCE 816 AA;
                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       646 LVEYPF 651
MIM; 164400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLVRA OR BLVR.
                                                                                                                                                                                                                                                                                                                                                                              3 LVEYPF 8
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-1- SIMILARITY: TO E.COLI YHHX.
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
MEDLINE-9314333; PubMed=8424666;
MEDLINE-93143333; PubMed=8424666;
Maines M.D., Trakshel G.M.;
"Purification and characterization of human biliverdin reductase.";
Arch. Biochem. Biophys. 300:320-326(1993).
                                                                                                                                                                                                                                                               Eukaryota, Euthazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutharia, Primates, Catarrhini, Hominidae, Homo.
                                                                                                       ö
                                                                                                                                                                                                                                                                                                    TISSUB-PLEACHE,
TISSUB-PLEACHE,
MEDLINE-96202961; PubMed-8631357;
MAINES M.D., Polevoda B.V., Huang T.-J., McCoubrey W.K. Jr.;
"Human biliverdin IXalpha reductase is a zinc-metalloprotein.
Characterization of purified and Escherichia coli expressed
                                                                                  Score 32; DB 1; Length 295; Pred. No. 39; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-117 FROM N.A.
Cordes M., Wollam C., Carter T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Komuro A., Tobe T., Nakano Y., Yamaguchi T., Tomita M.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                219C8EA96C150588 CRC64;
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
C->A: LOSS OF ACTIVITY.
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
                                                                                                                                                                                    296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 3-36, 48-74 AND 228-248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE=95014177; PubMed=7929092;
                                                                33565 MW;
                                                                                 Similarity 85.7%;
6; Conservative
                                                                                                                                                                                    STANDARD;
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279
280
291
292
73
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295 AA;
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                                                                                        Local Similarity
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                                                                                                                    3 LVEYPFT 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
A -> T (IN REF. 2).
B -> AG (IN REF. 2).
D -> B (IN REF. 2).
W, ODFD3B386F4DFCOA CRC64;
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Pred. No. 39;
0; Mismatches
                                                                                                                                                                                        EMBL; X93086; CAA63635.1; -.
EMBL; U34877; AAC35588.1; -.
EMBL; AC005189; AAC25526.1; -.
Genew; HGNC:1062; BLVRA.
MIM; 109750; -.
InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR000683; GFO_IDH_MOCA.
CAIdoreductase; NAD; NADP; Zinc.
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Matches 6; Conservative
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292
293
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95 LVEYPMT 101
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Search completed: April 22, 2003, 12:51:48 Job time : 5.5 secs

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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative calmodulin-binding protein.
Ar4631000, F6118,90 OR A74631000.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NUSI_TAXID=3702;
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09XNWB
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Q8W454;
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 April 22, 2003, 12:47:43 ; Search time 18 Seconds (without alignments) 103.024 Million cell updates/sec
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             GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

RA Garninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kin C., Lam B., Lin J.

RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Safou M.,

RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.; Theologis A.; Theologis A.;

"Arabidopais Full Length cDNA Clones.";

RI Shabi, AX062856; AAL32934.1;

RE SHBL; AX062856; AAL32934.1;

SEQUENCE 278 AA; 31406 MW; 398DCFB65C85A836 CRC64; SOUTBNICE FROM N.A.
SOUTBNICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J. Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakuruai T., Sakou M., Sahinn P., Yamada K., Shinozaki K., Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

Q8w454 arabidopsis Q65550 arabidopsis Q9b313 neoceratodu Q9m34 bothriomym Q9xxv9 delomys dor Q9xxv5 scapteromys Q9xxv0 reithrodon Q9cg14 cervus elap Q9tf12 spermophilu Q9tf11 spermophilu Q9tG08 spermophilu Q9tG08 spermophilu Q9tG08 cervus timo Q94c8 cervus turi Q94c8 cervus turi

Q8W454 Q65550 Q9B313 Q9MP34 Q9XNV8 Q9XNV0 Q9TG44 Q9TF64 Q9TF12 Q9TF11

110 110 88 88 88

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Formicidae, Dolichoderinae, Bothriomyrmex.
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Pred. No. 6.8;
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Last annotation update)
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(TrEMBLrel. 19, I
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Best Local Similarity
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"Augeralian lungfish (Neoceratodus forsteri) have low genetic
diversity at alloyme and mitochondrial loci: A conservation alert for
a living fossil?";
Conserv. Genet. 0:0-0(2001)
-!** FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sanctation update)
Putative calmodulin-binding protein.
FGI18.90 OR AT4G3100.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicocyledons; core eudicots; Rosidae; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                Gaps
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Bevan M., Benea V., Rechmann S., Borkova D., Ansorge W., Hoheisel
Mewes H.M., Mayer K., Schueller C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Dipnoi, Ceratodontiformes; Ceratodontidae; Neoceratodus.
NCBI_TaxID=7892;
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                1; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AA.
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                                                                                                          467 AA.
    Pred. No. 14;
1; Mismatches
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    Best Local Similarity 75.0%;
Matches 6; Conservative
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SEQUENCE FROM N.A.

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SEQUENCE TO N.A.

"Phylogenetic relationships and the radiation of sigmodontine rodents
"The South America: Evidence from cytochrome b.";

J. Mammal. Evol. 6.89-128(1999).

-!- FUNCTION: COMPLEX II OR CYTOCHROME B-CI CONVLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNHERSIS (BY SIMILARITY).

COUPLED TO ATP SYNHERSIS (BS SIMILARITY).

COUPLED TO ATP PROTEIN (BY SIMILARITY).

COUPLE SHALL THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,

CYTOCHROME C1 AND THE RIESEE PROTEIN (BY SIMILARITY).

CHESTIC STALLARITY: BELONGS TO THE CYTOCHROME B FAMILY.

CHESTIC STALLARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL, APRO032; CYTOCHROME D. C;

PREMI, PRO0032; CYTOCHROME D. C;

REMBL, PRO0033; CYTOCHROME D. N;

REAM; PRO0033; CYTOCHROME D. N;

REMBL, PRO0033; CYTOCHROME D. N;

REMBL, PRO0033; CYTOCHROME D. N;

REMBL, PRO0033; CYTOCHROME D. N;

REMBL PROPORTINE D. N;

REMBL PROPORTINE D. N;

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Smith M.F., Patton J.L.;
Smith M.F., Patton J.L.;
Pathonally selected and the radiation of sigmodontine rodents
"Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Exidence from cytochrome b.";
J. Mammal. Evol. 6:89-1281(1999).
---- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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PROSITE; PS00193; CYTOCHROME B QO; UNKNOWN 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 8; Length 352;
Pred. No. 29;
0; Mismatches 1; Indels
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SEQUENCE 352 AA; 39631 MW; AA408DB627140D6C CRC64;
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                                                                                                                                                                 Delomys dorsalis (striped Atlantic forest rat).
                                       352 AA.
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                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, CYtochrome B (Fragment).
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                                     PRELIMINARY;
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NCBI_TaxID=89126;
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                                   Q9XNV8
                                                       9VNX60
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RESULT 5
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Smith M.F., Patton J.L.,

Smith M.F., Patton J.L.,

"Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Bvidence from cytochrome b.";

J. Mammal. Evol. 6:89-128(1999).

- !- FUNCTION: COMPUENT II OR CYTOCHROME B.-CI COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERALES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

- COFACTOR: TWO HEME GROUPS (BSCS AND BSCS) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CYTOCHROME CI AND THE RIESKE PROTEIN (BY SIMILARITY).

- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL; AF108694; AAD45476.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                      Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
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Pfam; PF00032; cytochrome b C; 1.

Pfam; PF00033; cytochrome b N; 1.

PROSITE; PS00192; CYTOCHROME B HEME; 1.

PROSITE; PS00193; CYTOCHROME B QO; UNKNOWN 1.

Blectron transport; Heme; MiCochondrion; Respiratory chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 87.5%; Score 36; DB 8; Length 377; Similarity 87.5%; Pred. No. 31; 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   NON TER 1 1 SEQUENCE 377 AA; 42392 MW; 692D67AE20B6F3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 377 AA; 42533 MW; 618DB37396EE6E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 OPVEYPFT 344
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Transmembrane.
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Subjective phylogeny of ground squirrels and prairie dogs.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

COMPLEX (COMPLEX IO TOF THE UBIQUINOL-CYTOCHROME C REDUCTASE

- FUNCTION: COMPLEX II OR CYTOCHROME B.-CI COMPLEX). WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COMPLED TO APP SYNTHESIS (BY SIMILARIY).

C-I- COPACTOR: TWO HEME GROUPS (BS62 AWICH ARE NOT COVALENTLY)

C-I- COPACTOR: TWO HEME GROUPS (BS62 AWICH ARE NOT COVALENTLY)

C-I- SUBMINIT: HER ALIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,

C-I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C-I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C-I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

BREL, AFISTS887, AADSOITI...; -.

BREL, AFISTS887, AADSOITI...; -.

BREL, AFISTS887, CYTOCHROME B HEME; 1.

R PROSITE; PS00193; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammallai, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae, Spermophilus.

NCBI_TAXID=99842,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.0%; Score 36; DB 8; Length 379; Best Local Similarity 87.5%; Pred. No. 31; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 AA; 43024 MW; 1F115AE16850F5AA CRC64;
  Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermophilus madrensis (Sierra Madre ground squirrel).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 379 AA.
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SEQUENCE 37
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SEQUENCE 37
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Cervus.
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NCBI_TaxID=100390;
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75.0%; Score 36, DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels
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Last annotation update)
                                                                                                                                                                                OSTGL4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 379 AA
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Mitochondrion.
                                                                                                                                                                                                                                                                                                                     Cervus elaphus (Red deer).
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338 QPVEYPFT 345
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"A molecular phylogeny of ground squirrels and prairie dogs.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COPPACTOR: TWO HEMB GROUPS (BSE2 AND BSE6) WHICH ARE NOT COVALENTLY
--- COPPACTOR: TWO HEMB GROUPS (BSE2 AND BSE6) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SEY1069;
Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
Bogdanowicz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 87.5 Matches 7; Conservative
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       MCBI_TaxID=100390;
                                                                                  SEQUENCE FROM N.A.
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LE Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.

-I-FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE.

COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-I-COPACTOR: TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-I-SUBMLIT: THE MAIN SUBMITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESER PROTEIN (BY SIMILARITY).

-I-SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL, ARIPST991; AADS50231.1; -..

REMBL, RE17994; AADS50231.1; -..

REMBL, RE17994; AADS50231.1; -..

REMBL, RE17994; AADS50231.1; -..

PRAM: PRO013; CYTOCHROME B HEME; 1..

PRAM: PRO013; CYTOCHROME B HEME; 1..

PROSITE; PRO0193; CYTOCHROME B HEME; 1..

PROSITE; PRO0193; CYTOCHROME B HEME; 1..

PROSITE; PRO0193; CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

PROSITE; PRO0193; CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

PROSITE; PRO0193; CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

RESPECTION THE RESPONDED TO THE CYTOCHROME B HEME; 1..

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
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       8; Length 379
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                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S., Bogdanowicz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermophilus madrensis (Sierra Madre ground squirrel).
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Last annotation update).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 AA.
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       Score 36; DB 8
Pred. No. 31;
0; Mismatches
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       75.0%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 87.5
Matches 7; Conservative
Query Match 75.0
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                    341 QPVEYPFT 348
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Q9TF08
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Q9TF11
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Gaps

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75.0%; Score 36; DB 8; Length 379; 87.5%; Pred. No. 31; tive 0; Mismatches 1; Indels

42994 MW; 767009AD223C18AD CRC64;

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SEQUENCE FROM N.A.
STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M.F.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
-- COMPLEX (COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                           SEQUENCE OF 1-267 FROM N.A.
STRAILS-UMZ CAPALOG # 133965; TISSUB=LIVER;
Smith N.F., Patton J.L.;
Diversification of South American murid rodents: Evidence from
                                                                                                                                                                                                                                                                                                                mitochondrial DNA sequence data for the akodontine tribe."; Biol. J. Linn. Soc. 50:149-177(1993).
                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
PRT;
                                                                                                                      Akodon toba (Chaco grass mouse).
PRELIMINARY;
                               01-NOV-1996 (TrEMBLrel.
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PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                   379 AA; 42766 MW; 8B74E09004D8E663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 22, 2003, 12:53:49
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                                                                                      Transmembrane.
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Q94QC8;
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AC 0944000
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Subilited (JUL-1999) to the EMBL/GenBank/DDBJ databases.

L Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

COMPLEX (COMPLEX II OR CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C.1 COMPLEX), WHICH IS A COMPLEX OF SYNTHERSIS (BY SIMILARITY).

COMPLEX TO ATE SYNTHERSIS (BY SIMILARITY).

COUPLED TO ATE SYNTHERSIS (BY SIMILARITY).

COUPLED TO ATE SYNTHERSIS (BY SIMILARITY).

COPPACTOR: TWO HEME GROUPS (BS-52 AND BS-66) WHICH ARE NOT COVALENTLY CC. -1 SUBUNIT: THE MAIN SUBUNITS OF COMPLEX BY SIMILARITY).

COPPACTOR: THE PROTEIN (BY SIMILARITY).

COPPACTOR: THE RIBERE PROTEIN (BY SIMILARITY).

COPPACTOR: THE RIBERE PROTEIN (BY SIMILARITY).

COPPACTOR: THE RIBERE PROTEIN (BY SIMILARITY).

COPPACTOR: THE PROTEIN (BY SIMILARITY).

COPPACTO
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COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

--- CORACTOR: TWO HEME GROUPS (BS62 AÅD BS66) WHICH ARE NOT COVALENTLY BROUND TO THE PROTIENT (BY SIMILARITY).

--- SUBLINIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

--- SIMILARITY: BELOMOGS TO THE CYTOCHROME B FAMILY.

--- SIMILARITY: BELOMOGS TO THE CYTOCHROME B FAMILY.

INTERPRO, 1PRO00179; Cyt b. b.

PÉAM: PF00013; CYtochrome D. C; 1.

PÉAM: PF00013; CYTOCHROME D. C; 1.

PROSITE: PS00192; CYTOCHROME B HEME; 1.

PROSITE: PS00193; CYTOCHROME B HEME; 1.
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STRAIN=USNM CATALOG # 560661; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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STRAIN=USNM CATALOG # 560661; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Diversification of South American murid rodents: Evidence from mitochondrial DNA sequence data for the akodontine tribe.";
Biol. J. Linn. Soc. 50:149-177(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 379;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 75.0%; Score 36; DB 8; Local Similarity 87.5%; Pred. No. 31; Nes 7; Conservative 0; Mismatches
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STRAIN=USNM CATALOG # 560661; TISSUE=LIVER;
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(TrEMBLrel. 12,
(TrEMBLrel. 19,
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01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=100644;
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Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
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Q33940;
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Matches
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A Ludt C.J., Kuehn R., Schroeder W., Rottmann O.;

In Phylogeny of Cervidae based on mitochondrial genes.";

In Phylogeny of Cervidae based on mitochondrial genes.";

In Shuitted (SER-2001) to the EMBL/GenBank/DBL databases.

COMPLEX (COMPLEX III OR CYTOCHROME B.C. TOCHROME C.C.

COMPLEX (COMPLEX III OR CYTOCHROME B.C. TOCHROME B.C. TOCHROME D.C. TOCHROME C.C. TOCHROME D.C. TOCHROME D.C. TOCHROME D.C. TOCHROME D.C. TOCHROME D.C. TOCHROME D.C. TOCHROME C.C. TOCHROME D.C. TOC
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                                                                                                                                                          Gaps
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ammalia; Butheria; Cecartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
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                                                   Length 379
                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                   Score 36; DB 8;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 AA
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervus timorensis macassanicus.
                                                   75.0%;
87.5%;
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Conservative
Query Match
Best Local Similarity 87.59,
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es 7; Conserv
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Human WSX receptor Insulin/insulin-li Human BLyS binding Human BLyS binding Single chain Fv re Sil-VEGF2 construc

S11-scVEGF2 constr 2G3 hybridoma VL d Protein involved i

> AAY90813 AAY36951 AAG27700 AAG27699

AAB10863 AAB10864 AAY92171 AAY92164 AAW28154 ABP40069

AAR30450 ABB36950 AAG93597

AAR34019 AAR59513 AAY90819 AAR33954 AAR33951

Light chain CDR3 o Variable domain of Variable domain of Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Murine 13H10 light Murine 13H10 light Amino acid sequenc Staphylococcus epi S. epidermidis ope C242:11 Mahk kappa Peptide #4456 enco Human anti-Rh(D) c Bw 835 VK. Synthe Sequence of the ma 260F9 hybridoma VL

gil variable domai CTMO1 VL. Synthet Sequence of the li Sequence of the li CDR-grafted humani MAD CT-M-01 light gil2 variable domai Human polypeptide

> AAR59511 AAW29754 AAY56874

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Light chain CDR L3
Humanised anti-CD2
Mouse anti-EAb-42
Murine anti-EAb-42
Mouse MAb 2E12 L
Light (kappa) Chai
Light chain CDR3 o
Light chain CDR3 o
Light chain CDR3 o
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                                                                                                   April 22, 2003, 12:45:19 ; Search time 22.8214 Seconds (without alignments) 52.550 Million cell updates/sec
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| SIDSS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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             GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY32261
AAY32261
AAY70790
AAY70790
AAX12232
AAX12354
AAW398823
AAW39882
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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CD23; FCERII; IgB receptor; monoclonal antibody; Cl1; mouse; monoclonal antibody; chimerac antibody; humanised antibody; commondation; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; inflammation; arthritis; lupus erythematosus; multiple sclerosis; urticaria; nephrotic spandrome; glomerulonephritis; dermatitis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; sinflammatory bowel disease; ulcerative colitis; Crohn's disease; graft-versus-host disease; COPD; bronchitis; diabetes; hsullitis; ezzema; insulitis; B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                            Light chain CDR L3 of mouse anti-CD23 MAb C11.
ALIGNMENTS
                                                                                                                                                               AAY32256 standard; Peptide; 9 AA.
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Region
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                                                                                                                                           This sequence represents complementarity determinating region 3 (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY3262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY3224-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupue reythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveltis, dermatifis, psoriasis, unitiple sclerosis, diabetes, uveltis, dermatifis, psoriasis, unitiple sclerosis, csyndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, 5jogren's syndrome, allergies, allergic schma, intrinsic asthma, acute asthmatic execerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly type I (particularly thronic bronchitis) or diabetes (particularly type I (or studying interactions between CD23 and various ligands and cermining the binding agents.
                                                                     Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD23; FCERII; IgE receptor; monoclonal antibody; CII; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementearity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; urticaria; nephrotic syndrome; glomerulonephritis; crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; grafţ-versus-host disease; COPD; bronchitis; diabetes;
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Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 48; DB 21; Length 9 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-CD23 MAb C11 light chain variable region.
Bonnefoy JMP, Crowe SJ, Ellis JH, Kapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "framework region 2"
55..61
/note= "CDR 2"
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/note= "framework region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32262 standard, Protein, 116 AA.
                                                                                                                   Claim 1; Page 40; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CDR 1"
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B-cell malignancy; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                           2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QQLVEYPFT 9
|||||||||
1 QQLVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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this sequence represents the light chain variable region (VL) of humanised anti-CD23 (PCERII) monoclonal antibody C11 composed of a human framework (HSTGRVII) and the light chain composed of a human framework (HSTGRVII) and the light chain complementarity determining regions (see AAY212254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, auch as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on human therapy, for the treatment of arthritis, and heavtpoictic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's fibyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergiaes, allergic sthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly thronic bronchitis) or diabetes (particularly type I colitis, dath, and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and certermining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shearin J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crowe SJ, Ellis JH, Rapson NT,
/note= "framework region 3"
94..102
/note= "CDR 3"
103..113
                                                                                                                                                region 4"
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                                                                                                                                             /note= "framework
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N-PSDB; AAZ34747.
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Matches 9; Conserv
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This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAY32262), which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32264-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble, CD33 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies allergic sthma, intrinsic asthma, as syndrome, allergies, allergic sthma, intrinsic asthma, as syndrome, inclusing schma, and eccema, graft-versus-host disease, COPD, insultis, bronchitis, cromying the Area of the season of diabetes), and B-cell malignancies (claimed). They are also useful disease, bind and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell receptor specific antibodies useful for treating e.g. arthritis
inflammation, arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; bernatitis; psoriasis; urticaria; nephrotic syndrome; glomerulomephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; inflammatory bowel disease; asthma; rhinitis; czemm; allergy; asthma; rhinitis; czemm; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                         83..92
/note= "CDR L2"
125..134
/note= "CDR L3"
                                                                                                                                                                                                          55..70
/note= "CDR L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 2; 81pp; English
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Murine, p53 protein, PAb-421, monoclonal antibody; mAb, IDI-1; anti-idiotypic antibody, DNA-binding domain, defamatological, immunosuppressive, antiinflammatory; autoimmune response; GLE, systemic lupus erythematosus; diagnosis; treatment; autoantigen; light chain variable region; VL; complementarity determining region; CDR.
                                                    Gaps
                                                    ;
0
                       93.8%; Score 45; DB 21; Length 19;
88.9%; Pred. No. 0.031;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Murine anti-PAb-421 IDI-1 mAb light chain variable region.
                                                                                                                                                                                  AAY70790 standard; Protein; 122 AA.
                                                                                                                                                                                                                                            (first entry)
                                                       Conservative
                                      Local Similarity
                                                                                               19 AA;
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                                                                                  1 QQLVEYPFT
                                                                                                                                                                                                                                         31-JUL-2000
                                                                                                                                                                                                                AAY70790;
Sequence
                          Query Match
                                           Best Loca
Matches
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Gaps

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100.0%; Score 48; DB 21; Length 145; 100.0%; Pred. No. 0.067; or Mismatches 0; Indels

Conservative

6

Matches

125 QQLVEYPFT 133

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1 QQLVEYPFT 9

Best Local Similarity

Query Match

AAY70804 standard; peptide; 19 AA.

AAY70804 ID AAY7 XX RESULT 4

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                                                                                                      Murine, p53 protein, monoclonal antibody, mAb; PAb-421; IDI-1; IDI-1 L3; light chain variable region; VL; complementarity determining region; CDR; dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLB; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
                                                                   Murine anti-PAb-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythematosus (SLE) by down-regulating the autoimmune response to the Cterminal DNA-binding domain of p53 protein by an active compound. The present sequence is a IDI-1 i3 peptide which comprises the complementarity determining region (CDR) of the light chain of IDI-1 monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic antibody Ab2 mAb specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide corresponds to residues 92-110 of IDI-1 light chain variable region. It is an example of the active compound useful in the diagnosis, prevention and treatment of SLE in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent discloses a method for the treatment of systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the protein by an active compound comprising of antibodies to p53 or
                                                                                                                                                                                                                                                                                                                                                                                                                                            Herkel J;
                                                                                                                                                                                 DNA-binding domain; anti-idiotypic antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rotter V, Erez-Alon N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 78; Fig 10; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                     98US-0104816.
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                                  31-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragments of p53
                                                                                                                                                                                                                                                          WO200023082-A1.
                                                                                                                                                                                                                                                                                                                                  19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                       19-OCT-1998;
                                                                                                                                                                                                                                                                                             27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen IR,
 AAY70804;
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Key Region Mus sp.

Region

Region

27-APR-2000

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The mouse VL gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.
                                                                                                                                                                                                                New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the light (kappa)- chain variable (V) region of a mouse monoclonal antibody (MAb), 2E12, and is specific for an HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%; Score 45; DB 12; Length 131;
88.9%; Pred. No. 0.24;
iive 1; Mismatches 0; Indels
                                                                                                                                 Ghosh-Dastidar P, Robinson RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain variable region of murine 2E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric antibodies; immunoconjugates; HIV; AIDS.
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                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 108pp; English.
                                90WO-US06627.
                                                                 89US-0433703.
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hes 8; Conservative
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                                                                                                                                   Horwitz AH,
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                                                                                                                                                                    WPI; 1991-178106/24
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 131 AA;
                                                                                                  (XOMA-) XOMA CORP.
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immunoglobulin.
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                               13-NOV-1990;
                                                                 13-NOV-1989;
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 30-MAY-1991.
                                                                                                                                   Better MD,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the c-terminal DNA-binding domain of Ep3 protein by an active compound. The present sequence is a light chain variable region of IDI-1 an anti-diotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on complementarity determining regions of light and heavy chain variable regions of these antibodies, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or
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                                                                                                                 58.64
/label= CDR
/note= "Complementarity determining region"
97.105
/label= CDR
/note= "Complementarity determining region"
                                                                17..42
/label= CDR
/note= "Complementarity determining region"
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                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 78; Fig 9; 87pp; English.
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19-AUG-1991

Mus sp.

AAR12232;

Sequence

Best Loca Matches

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Gaps

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AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
   viral antigen. It is used in the construction of a chimeric Mab comprising heavy and light chains having murine V regions and human C regions. The chimeric Mabs are more effective than murine Mab 2B12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (d) regions, to generate restriction enzyme recognition sites. The chimeric Mabs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.
                                                                                                                                                                                                                                                                     Gaps
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88.9%;
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Best Local Similarity 88.3"
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-077166/07.
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9 AA;

Sequence

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                                                                                                                                                                                                                                                                                 Variable domain, lambda light chain, catalytic antibody; degradation; cocaine, cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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Pred. No. 0.33;
0; Mismatches 1; Indels
Score 44; DB 19; Lengtn >; Pred. No. 7.88+05; Indels
                                                                                                                                                                                                                                                          Light chain of the catalytic antibody 2A10.
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                                                                                                                                                                        AAW39882 standard; Protein; 113 AA.
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88.9%;
               91.7%;
88.9%;
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               Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
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                                                                      1 QQLVEYPFT 9
                                                                                                  1 QOFVEYPFT 9
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AAW39804
ID AAW39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transitions state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic caid from 3H-phenyl cocaine, The 2AHO antibody (AAW39809 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AHO has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                             Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                Variable domain of the Kappa light chain of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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Pred. No. 0.33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Pages 73-74; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK.
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88.9%;
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                                               (first entry)
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                                                                                                                                                                   overdose; addiction.
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                AAW39804;
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Matches
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CCR2. They are useful for inhibiting or treating cortion of a cell expressing cCR2 autoimmune disorders such as rheumatory disorder, autoimmune disorders such as thermatory disorder, autoimmune disorders such as thermatory disorder, autoimmune disorders such as thermatory arthritis and multiple sclerosis, atherogenesis and atherosclerosis, arthritis and inthe manufacture of a medicament for treating CCR2 mediated alleratory chronic and acute inflammatory glomerulopathies, acquired mediated allerator reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired intervention, including angioplasty and/or stent placement in a mammal. CC Humanised antibodies are also useful for inhibiting narrowing of the lumanised antibodies are also useful for inhibiting narrowing of the lumanised antibodies are also useful for inhibiting nearming of a vessel in a mammal, preferably associated with vascular intervention.

The present sequence is mouse germline kappa light chain variable
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inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                     O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                     Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 151; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW39817 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                02-FEB-2001; 2001WO-US03537.
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Matches
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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable domain of the Kappa light chain of catalytic antibody 12H1.
                                                                                                                                                                                                                                                                New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Pages 71-72; 147pp; English.
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94 QHFVDYPFT 102
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31-DEC-1997.
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                                                                                                                                                                     Landry DW;
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                                    Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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66.7%; Pred. No. 7.8e+05;
iive 1; Mismatches 2;
  Light chain CDR3 of catalytic antibody 3B9
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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine pransition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release sh-benzoic acid from 3h-phenyl occaine. The 12H1 antibody (AAW39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                  New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 36; DB 19; Length 113; 66.7%; Pred. No. 13; ive 1; Mismatches 2; Indels
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96US-0585005.
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Matches 6; Conservative
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94 QHFVDYPFT 102
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                                                                    P-PSDB; AAV09802
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08-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24063;
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The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also differentiation of a cell expressing the WSX receptor. It can also intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or contake in an obese mammal. WSX receptor ligands can be used to sepecially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate marrow transplantation therapy. It can also be used to repopulate collocation disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, cardiovascular diseases, cardiovascular diseases, can cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 18; Length 241;
Pred. No. 30;
1; Mismatches 2; Indels ·
                     Example 14; Pages 122-123; 219pp; English.
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nes 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AA;
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Gaps

Sequence:

Run on:

Searched:

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77.1%; Score 37; DB 10; Length 100; 100.0%; Pred. No. 3.6; Live 0; Mismatches 0; Indels
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US-09-976-78-8
US-09-976-78-8
US-09-985-198-8
US-09-881-82-6
US-09-881-24-12613
US-09-815-242-5756
US-09-815-242-5756
US-09-815-242-5756
US-09-976-787-29
US-09-976-787-29
US-09-976-787-28
US-09-976-188-27
US-09-976-188-27
US-09-901-252-17
US-09-91-252-17
US-09-922-217-1118
US-09-918-18-248-4123
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
US-09-840-459-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
7; Conserva
   Sequence 32, Appl Sequence 130, Appl Sequence 1310, Appl Sequence 47635, A Sequence 40, Appl Sequence 4, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 745, Appli Sequence 745, Appli Sequence 23, Appli Sequence 24, Appli Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                  April 22, 2003, 12:53:59; Search time 9.48214 Seconds (without alignments) 76.055 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/USO8_NEW PUB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/USO0_PUBCOMB.pep:*
                    GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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1 US-08-779-457-50

9 US-09-880-748-936

10 US-09-848-758-40

10 US-09-64-761-47635

9 US-09-948-751-40

10 US-09-948-751-40

10 US-09-948-751-40

10 US-09-107-058-8

10 US-09-107-058-8

10 US-09-107-117-8

9 US-09-104-545-4

9 US-10-045-545-4

9 US-10-045-545-4

9 US-10-045-545-4

9 US-10-045-545-4

10 US-09-976-787-6

10 US-09-976-187-6

10 US-09-976-187-6
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              301932 segs, 80129803 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
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Match Length
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                                                                                    OM protein
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Maximum DB
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ALIGNMENTS

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Gaps

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QQLVEYP 7

В 8

RESULT

US-09-809-391-745 US-09-976-787-24 US-09-865-198-23

Result

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RESULT 5
US-09-864-761-47635
US-09-864-761-47635
Sequence 47635, Application US/09864761
Sequence 47635, Application US/09864761
GENERAL INFORMATION:
SAPLICANT: Penn, Sharion G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensher Browner, Chen, Wensher Browner, Chen, Wensher Browner, Chen, Wensher Browner, Chen, TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION UNMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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publication No. US20030059937A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT PILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-03-16
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLICATION NUMBER: 00/293,499
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 9; Length 251;
Pred. No. 14;
1; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/217,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1110
LENGTH: 251
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Best Local Similarity 66.7%;
Matches 6; Conservative
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US-09-880-748-936
                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-880-748-1310
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US-09-880-748-936
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US-09-880-748-1310

i Sequence 1310, Application US/09880748

i Sequence 1310, Application US/09880748

i Publication No. U52003005937A1

i GENERAL INFORMATION:

APPLICANT: Ruben Artibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PLILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,316

PRIOR APPLICATION NUMBER: 60/210,316

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16
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                   Sequence 50, Application US/08779457
Publication No. US20020193571A1
GENERAL INPORMATION
SEQUENCE 50, Application US/08779457
Publication No. US20020193571A1
GENERAL INPORMATION
APPLICANT: Chiang, Nancy Y.
APPLICANT: Chiang, Naincy Y.
APPLICANT: Chiang, Nailiam
APPLICANT: Matthews, William
APPLICANT: Grantech, Naince
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: California
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winball FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/79,457
FILING DATE: 06/20/96
FILING DATE: 06/20/96
FILING DATE: 06/20/96
FILING DATE: 01/08/96
FILING DATE: 10/08/96
FILING DATE: 10/08/96
FILING DATE: 10/08/96
FILING DATE: 10/08/96
FILING DATE: 11/252-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 241 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 QQLISYPLT 231
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US-08-779-457-50
       US-08-779-457-50
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Gaps

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Sequence 10, Application US/09973451

Sequence 10, Application US/09973451

Sequence 10, Application US/09973451

GENERAL INPORMATION:

APPLICANT: JACOBSON, Myron K.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: JACOBSON, Myron K.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: JACOBSON, Blaine L.

APPLICANT: AM, Jean-Christophe

TITLE OF INVENTION: GENERS ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE

TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES INMUNOREACTIV

TITLE OF INVENTION: THEREWITH

TITLE OF INVENTION: THEREWITH

FILE REFERENCE: 1000/9973,451

CURRENT FILING DATE: 2001-10-09

FRIOR PILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-05-01

NUMBER OF SEQ ID NOS: 38

LENGTH: 726

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Sequence 4, Application US/10164359

Publication No. US2030012776A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement

TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement

TITLE OF INVENTION: Stress

FILE REPERENCE: 601-1-1080S

CURRENT APPLICATION NUMBER: PCT/US00/33438

PRIOR APPLICATION NUMBER: PCT/US00/33438

PRIOR APPLICATION NUMBER: 60169,418

PRIOR FILING DATE: 2006-12-07

PRIOR FILING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                           Query Match 68.8%; Score 33; DB 9; Length 107; Best Local Similarity 66.7%; Pred. No. 23; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                OTHER INFORMATION: anti-Rh(D) chain 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
ORGANISM: Homo sapiens
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 QQLNSYPYT 96
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172 QELIEYP 178
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US-10-164-359-4
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Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SCRTING METHOD FOR PRODUCTION THEREOF
FILER REPERENCE: 09596-42U.
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: ERALIER APPLICATION NUMBER: 09/240,274
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-01-29
PRIOR PILING DATE: EARLIER FILING DATE: 1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.1

OTHER INFORMATION: EST HUMAN HIT: AW612517.1, EVALUE 7.00e-43

OTHER INFORMATION: SWISSPROT HIT: P54253, EVALUE 1.00e-43

US-09-864-761-47635
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   PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||
6 LVEYPF 11
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Gaps

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RESULT 11
US-09-144-886-97
Sequence 97, Application US/09144886
Setence 97, Application US/09144886
Setence 97, Application US/09144886
Setence 97, Application US/09144886
Setence No. US20020155114A1
SETENCE NO. US20020155114A1
SETENCE OF INVENTION: The rapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: The rapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Bottlinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT PRILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE Patentin Ver. 2.0
SEQ ID NO 97
LENGTH: 109
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US-09-144-886-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 32; DB 10; Length 105;
llarity 55.6%; Pred. No. 35;
Conservative 3; Mismatches 1; Indels
                                                                                                                                                 STATE: New York
COUMTRY: United States of America
ZIP: 10036
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/761,117
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.7%; Score 32; DB 9; Length 109; Best Local Similarity 55.6%; Pred. No. 36; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/43771-A-PCT-US-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELERX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Inhear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-761-117-8
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LENGTH: 105 amino acids
TYPE: amino acid
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ORGANISM: Artificial Sequence
                                          NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 5; Conserv
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72 QQILEYAYT 80
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Pred. No. 35;
3; Mismatches 1; Indel8
                                                                                                              Length 105;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09107058
Patent No. US20010010922A1
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Niu, Hui-Feng
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE DOCKET NUMBER: 0575/43771-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
TELEX: 42253 COOP UI
INFORMATION POR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISN PC compatible
COMPUTER: ISN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,058
FILING DATE:
CLASSIFICATION:
                                                                                                            Score 32; DB 9;
Pred. No. 35;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09761117
Patent No. US20010012887A1
GENERAL INFORMATION:
APPLICANT:
Chaganti, Raju S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-107-058-8
                                                                                                            66.7%;
55.6%;
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55.6%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 55.67
Then 5; Conservative
                                                                                                         Query Match
Best Local Similarity 55.6
Matches 5; Conservative
  ; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-359-4
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72 QQILEYAYT 80
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66 QQILEYAYT 74
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US-09-761-117-8
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RESULT 15
US-09-976-787-6
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Publication No. US20030027124A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: TISSUE
TITLE OF INVENTION: TISSUE
FILE REPERENCE: 176 60991;
CURRENT APPLICATION NUMBER: US/10/045,545;
FILE REPERENCE: 176 60991;
CURRENT APPLICATION NUMBER: 60/261,500;
PRIOR FILING DATE: 2002-01-12;
NUMBER OF SEQ ID NOS: 17;
SEQ ID NO 1;
IENGTH: 296
                                                                                                                                                                                                      Sequence 4, Application US/10045545;
Sequence 4, Application US/10045545;
Publication No. US20030027124A1
GENERAL INFORMATION: MAINEN
TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING;
TITLE OF INVENTION: TISSUE
FILE REFERENCE: 176/60941;
CURRENT APPLICATION NUMBER: US/10/045,545
CURRENT PILING DATE: 2002-01-14
PRIOR PILING DATE: 2002-01-12
SEQUENCE: PARCHE PATENTION OF SEQUENCE OF SEQUENCE
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US-10-045-545-3
i Sequence 3, Application US/10045545
j Publication No. US20030027124A1
GENERAL INFORMATION:
A PAPLICANT: Maines, Mahin D.
TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING;
TITLE OF INVENTION: TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 9; Length 295;
Pred. No. 98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 66.7%;
Similarity 85.7%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus
US-10-045-545-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                   90 QQYIGYPYT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 LVEYPMT 100
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1 QQLVEYPFT 9
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                                                                                                                                                                  RESULT 12
US-10-045-545-4
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US-10-045-545-1
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                                                                                                                                                               Score 32; DB 9; Length 296;
Pred. No. 98;
0; Mismatches 1; Indels
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Pred. No. 2.7e+05;
0; Mismatches 3; Indels
FILE REFERENCE: 176/60981
CURRENT APPLICATION NUMBER: US/10/045,545
CURRENT FILING DATE: 2002-01-14
FRIOR APPLICATION NUMBER: 60/261,500
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3
LENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 22, 2003, 13:11:13 Job time : 10.4821 secs
                                                                                                                                                                   Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-09-976-787-6
                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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A; Molecule type: mRNA
A; Residues: 1-17 - <4DF.
C; Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-leva:
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 33; DB 1; Length 117; Best Local Similarity 100.0%; Pred. No. 26; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                      April 22, 2003, 12:48:24; Search time 4.91071 Seconds (without alignments) 97.882 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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T28818
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D84505
S39978
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G2MSU1
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T42185
AE1752
AH1728
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hypothetical prote cation efflux syst cadmium, zinc, cob SWI/SNF family hel helicase, SMEZ/Radmultidrug resistan hypothetical prote Ig heavy chain V r Ig heavy chain pre hypothetical prote Ig heavy chain pre	Si	ted] - Halobacterium sp. NRC-1 on 02-Feb-2001 #text_change 02-Feb-2001 G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab. 176-12181, 2000 ennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; lerium species NRC-1. 04483; PMID:11016950	DB 2; Length 67; 15; 0; Indels 0; Gaps 0;	RESULT 2 GZMSU1 Ig heavy chain V region (UPC10) - mouse C;6pecies: Mus musculus (house mouse) C;botacis: 0.3-Aug-1984 #sequence_revision 0.3-Aug-1984 #text_change 23-Mar-2001 C;Accession: A02081 R;Auffray, C.; Sikorav, J.L.; Ollo, R.; Rougeon, F. Ann. Immunol. (Paris) 132D, 77-88, 1981. Ash:Title: Correlation between D region structure and antigen-binding specifity: evidency A;Reference number: A02081; MUID:83021113; PMID:6181731 A;Accession.
747495 743430 743830 744700 786595 742029 742029 742029 713692 813690 813690 813691 813691 813691 813691 813691	ALIGNMENTS	1 1 1 1 1 1 1 1 1 1	Score 33; D Pred. No. 15 0; Mismatches	mouse use) ision 03-Auc o, R.; Rouge yion structu 83021113; PR
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00000000000000000000000000000000000000		RESULT 1 A84376 hypothetical protein Vng2253h [impor' Cispecies: Halobacterium sp. NRC-1 Cispecies: Halobacterium sp. NRC-1 Cispecies: Or-Eeb-2001 #sequence_revision Cispecession: A64376 Fund, W. J. Kennedy, S. P. J. Mahairas, J. Leithauser, B. J. Keller, K. J. Cruz, Jung, K. H. J. Alam, M. J. Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 7. 12 A. Alathors: Hou, S. J. Daniels, C. J. J. DA, Altie: Genome sequence of Halobact, A. Reference number: A84160; MUID:205. A. Residues: preliminary A. Rocession: A84376 A. Scatus: preliminary A. Rocession: A84376 A. Residues: 1-67 < STO. A. Residues: 1-67 < STO. A. Residues: 1-67 < STO. C. Gentics: A84377; NID C. Gentics: A84377; NID C. Gentics: A84377; A. A. Genetics: A84374; A. A. A. Genetics: A84375; A. A. Genetics: A. A. Genetics: A84375; A. Genetics: A84375	Query Match Best Local Si Matches 5;	RESULT 2 GAMSU1 Ig heavy chain C;Species: Mus C;Date: 03-Aug- C;Accession: Ab An. Immunol. (A, Title: Correl A, Affitle: Correl A, Reference num A, Accession: Ab
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Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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T42185
Conserved hypothetical protein L7085 - Escherichia coli plasmid pol57
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accesgion: T42185
R;Burland, V.; Ashao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher
                                                                                                                                                                                     Citrate transport protein - Klebsiella pneumoniae plasmid pES1
N;Alternate names: citrate carrier
C;Species: Klebsiella pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C;Accession: S09681
R;van der Rest, M.E.; Schwarz, E.; Oesterhelt, D.; Konings, W.N.
Eur. J. Biochem. 189, 401-407, 1990
A;Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.
A;Reference number: S09681
A;Molecule type: DNA
A;Residues: 1-444 «RES>
A;Cross-references: EMBL:X51479; NID:943800; PIDN:CAA35844.1; PID:943801
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: citrate utilization determinant
C;Superfamily: citrate utilization determinant
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hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria
C;Species: P:; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Domes, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Atitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; Mulb:21537279; PMID:11679669
A;Accession: AE1752
A;Acces
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C; Species Listeria innocua (strain Clip11262)
C; Species Listeria innocua
C; Date: 27-Nov-2001
C; Accession: Ah1728
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A; Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MuID:21537279; PMID:11679669
A; Accession: AH1728
A; Accession: AH1728
A; Residues: 1-298 cGLA>
A; Residues: 1-298 cGLA>
A; Residues: 1-298 cGLA>
A; Residues: Listeria Clip11262
C; Genetics:
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A;Reference number: Z22068; MUID:98391744; FMID:9722640
A;Accession: T42185
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Vipe: DNA
A;Residuse: 1-86 <br/>A;Residuse: 1-86 <br/>A;Cross-references: EMBL:AF074613; PIDN:AAC70153.1<br/>A;Experimental source: strain EDL933; serotype O157:H7<br/>A;Genetics: plasmid pO157<br/>A;Note: L7085
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Pred. No. 69;
1; Mismatches
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C;Species: Pseudomonas aeruginosa ceruginosa (strain PAOI)
C;Species: Bseudomonas aeruginosa cruginosa circain PAOI)
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E3163
Estover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
A;Aritle: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathox A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                            Cispecies: Pseudomonas aeruginosa
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: H83554
R;Stower, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule_type: DNA_A;Residues: 1-358 <STO>A;Residues: 1-358 <STO>A;Residues: 1-358 <STO>A;Coss-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001A;Experimental source: strain PAO1C;Genetics: A;Gene: PA0736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                Nypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
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R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 30; DB 2; Length 358; 80.0%; Pred. No. 2.7e+02; ive 1; Mismatches 0; Indels
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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A;Experimental source: fetal kidney; clone DKFZp566D213
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Best Local Similarity 80.0%;
Matches 4; Conservative
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A;Accession: T08724
A;Molecule type: mRNA
A;Residues: 1-417 <KOE>
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Best Local Similarity
Matches 4; Conserva
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A;Molecule type: DNA
A;Residues: 1-375 <STO>
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19 GYWLS 2
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Carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Accession: H86836
C;Accession: H86836
C;Accession: H86836
C;Accession: H86836
C;Accession: H86836
C;Accession: H86836
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: B03A
A;Status: preliminary
A;Molecule type: DNA
A;References: GB:AE005176; PID:g12724712; PIDN:AAK05794.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: phosphotransferase
C;Keywords: phosphotransferase
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C;Species: Methanobacterium thermoautotrophicum (strain Delta H)
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
R;Accession: 669142
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
i Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69142
A;Accession: G69142
A;Accession: G69142
A;Accession: G69142
A;Accession: G69142
A;Residues: 1-348 <ATT->
A;Accession: A
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G69142
GDP-D-mannose dehydratase - Methanobacteríum thermoautotrophicum (strain Delta H)
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Pred. No. 2.4e+02;
1; Mismatches 0; Indels
                                                                                     Length 298;
                                                                            90.9%; Score 30; DB 2; Length 298
80.0%; Pred. No. 2.3e+02;
ive 1; Misma#ches 0; Indels
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C;Superfamily: GDP-D-mannose dehydratase
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Best Local Similarity 80.0%;
Matches 4; Conservative 1
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Best Local Similarity
Matches 4; Conserv
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156 GYWMT 160
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45 GYWLS 49
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A; Gene: lin2373
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undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycete. C;Species: Actinobacillus actinomycetemcomitans
C;Species: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession. T00113
R;Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcom A;Reference number: Z14111; MUID:99023768; PMID:9805002
A;Accession: T00113
A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 1-452 «NAK»
A;Crosar references: EMBL;AB010415; NID:g3132248; PIDN:BAA28142.1; PID:g3132265
A;Experimental source: strain NCTC 9710
C;Superfamily: xps2A protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                PTS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae (5)Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 S;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6) ("Species: Streptococcus pneumoniae ("Species: Streptococcus pneumoniae ("Species: Streptococcus pneumoniae ("Species: 20-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 ("Sociession: G9813 R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. R. Hoskins, J.A.; Alborn Jr., W.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Althoris: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Atters: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Accession: G98113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 < KUR>
A;Residues: 1-448 < KUR>
A;Residues: 1-448 < KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00740.1; PID:g15459636; GSPDB:GN00174
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A;Molecule type: DNA
A;Residues: 1-448 cKUR>
A;Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:g14973641; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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                                                                                Length 417;
                                                       Score 30; DB 2; Length 41.7
Pred, No. 3.16+02;
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Pred. No. 3.3e+02;
1; Mismatches 0; Indels
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80.0%; Pred. No. 3.1.
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                                                                                                                                     4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
C;Genetics:
A;Note: DKFZp566D213.1
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402 GYWLS 406
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A,Gene: SP2129
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                 P94532
P45243
P08395
Q50614
Q01745
Q00854
Q008894
Q00899
Q006399
P04939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M36631; AAA38078.1; -.
PIR; A02081; GZMSU1.
INTESP: PO1810; ZFBJ.
INTESP: PO1810; ZFBJ.
INTESP: PO1803596; Ig_WHC.
INTESP: SM00406; IGV; I.
IMMUNICALOUDIN V region.
NON TER
NEW TAX 117 AA; 13001 MW; B20A1074F8E99E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 heavy chain V region UPC10.
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PH84 YEAST
CSTA_BACSU
SPRA_BACSU
SPRA_ECOLI
Y119 WYCTU
GAOA DACDE
YQVS_CREEL
VP4 ROTPG
VP7 ROTPG
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CIT1 KLEPN
ID CIT1 KLEPN STANDARD; 1
AC P16482;
DT 01-AUG-1990 (Rel. 15, Created)
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                                                                                                                                  April 22, 2003, 12:46:53 ; Search time 2.5 Seconds (without alignments) 82.953 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                                                                                                                             112892 segs, 41476328 residues
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CIT1 KLEPN.
CAPA KLULA
AMPR PROST
ARCC ENTFC
ARCD LACSK
ARCD CLOPE
PTSB STAXY
SYG AERPE
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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33
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RESULT 4
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                                                                                                                                                                                                                                                   (1) ESGUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 13882;

MEDLINE=90249385; PubMed=2186908;

MEDLINE=90249385; PubMed=2186908;

MEDLINE=90249385; PubMed=2186908;

A van der Reet W.B., Schwarz B., Oesterhelt D., Konings W.N.;

I DAR, Sequence of a citrate carrier of Klebsiella pneumoniae.";

Bur. J. Biochem. 189:401-407(1990).

I Bur. J. Biochem. 189:401-407(1990).

I THE CONCONITANT EXPORT OF A PROTON (SYMPORT SYSTEM).

I THE CONCONITANT EXPORT OF A PROTON (SYMPORT SYSTEM).

C -1- PATHWAY: ALLOWS THE UTILIZATION OF CITRATE AS A SOLE SOURCE OF CARBON AND EDRERO.

C -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

C -1- SIMILARITY: TO CIT IN TN3411 AND PWR60 FOUND IN E.COLI AND TO CIT IN COLI AND TO CIT AND 
                                                                                                                                       Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cltrate-proton symporter (Citrate transporter) (Citrate carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; Transmembrane; Inner membrane; Citrate utilization;
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llarity 100.0%; Pred. No. 34;
Conservative 0; Mismatches 0; Indels
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6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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D431F732EEDA3EC2 CRC64;
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InterPro; IRR004736; Cit H symport.
InterPro; IRR00436; Sub transporter.
Pfam; PF00083; sugar_tr; I.
PIGREPM; TIGRO0883; Solude; 1:
PROSITE; PS00116; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00117; SUGAR_TRANSPORT_2; 1.
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"DNA sequence of the SFT1 gene from Kluyveromyces lactis.";

submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: P-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT

MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)

THEREBY BLOCKING THE EXCHANGE OF SUBMINTS AT THESE ENDS. UNLIKE

OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE

PROTEINS DO NOT SEVER ACTIN FILAMENTS (BY SIMILARITY).

-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis (Yeast).
Bukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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InterPro; IPR002189; F-actin cap_A.
InterPro; IPR001919; F-actin cap_A.
PRINTS; PR00191; FACTINCAPA.
PRODOM; PD006960; F-aCTIN cap_A; 1.
PROSITE; P800749; F-ACTIN CAPPING_A.;
PROSITE; P800749; F-ACTIN CAPPING_A.;
ACTIN Lbinding; Capping protein.
NON TER
SEQÜENCE 214 AA; 24380 MW; 31851D6573630C02 CRC64;
                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
F-actin capping protein alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPR PROST STANDARD; PRT; 292 AA. 069772; 30-MXY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Transcriptional activator protein ampR.
                                                                                                                                                                                       214 AA
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28985;
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                                               415 GYWWS 419
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CAPA KLULA
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NCBI_TaxID=1599;
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86 GYWLS 90
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Matches
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                                                                                             Koeck J.L., Baemaciogullari S., Parzy D., Barnaud G., Teyssou R., Buisson Y., Philippon A., Arlet G.J.;

"Cloning and sequencing of ampC and ampR genes from Providencia stuartii.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION OF BETA-LACTAMASE (AMPC).

-!- SUBCELJULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecium (Streptococcus faecium), and
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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MEDLINE=94141928; PubMed=8308897;
Marina A., Bravo J., Fita I., Rubio V.;
"Crystallization, characterization and preliminary crystallographic
studies of carbamate kinase of Streptococcus faecium.";
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Marina A., Uriarte M., Barcelona B., Fresquet V., Cervera J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.9%; Score 30; DB 1; Length 292; 80.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00847; HTH LyBR.
InterPro; IPRO0119; LyBR_subst.
Pfam; PF004065; HTH 1; 1.
Pfam; PF034065; LyBR_substrate; 1.
PROSITE; PS00049; HTH LYBR. FMILY; 1.
PROSITE; PS00044; HTH LYBR. FMILY; 1.
PROSITE; PS00048; HTH LYBR. FMILY; 1.
PROSITE; PS00048; HTH LYBR. FMILY; 1.
PROSITE; PS00049; HTH LYBR. FMILY; 1.
PS00049; HTH LYBR. F
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Best Local Similarity
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                                                             SEQUENCE FROM N.A.
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                       NCBI_TaxID=588;
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  Providencia
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                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=98361904; PubMed=9696763;
Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.;
Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.;
Zuniga M., Champomier analysis of the gene cluster encoding the enzymes of the arginine deiminase pathway of Lactobacillus sake.";
J. Bacteriol. 180:4154-4159(1998).
AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENREGY CONVERSION IN THE AND ORNITHINE DEIMINASE PATHWAY (BY SIMILARITY).
SIBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                      phosphate.
--- PATHWAY: Arginine degradation via arginine deiminase; third step.
---- SUBUNIT: HOMODIMER (PREDOMINANTLY) AND HOMOTETRAMER.
---- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
---- SIMILARITY: BELONGS TO THE CARBAMATE KINASE FAMILY.
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J. Mol. Biol. 235:1345-1347(1994).
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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309 AA; 32795 MW; 5014514A7FEEB290 CRC64;
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I -> D (IN REF. 2).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AJ223331; CAA11270.1; -.
EMBL; AJ223332; CAA11271.1; -.
PIR; S44002; S44002.
HSSP; S95474; IR19.
InterPro; IPR001048; Aa_Kinase.
InterPro; IPR003964; Bac_carb_kinase.
InterPro; IPR003964; Bac_carb_kinase.
INTERFAMS; TIGR00746; arCC; 1.
Transferase; Kinase; Arginine metabolism.
CONFLICT 33 157 MISSING (IN REF.
CONFLICT 168 168 I -> D (IN REF.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@1sb-sib.ch).
                                                                     EMBL; AP003185; BAB79876.1; -.
InterPro; IPR002293; AA/Fel_Drmeasel.
InterPro; IPR004841; Permease.
InterPro; IPR004754; R/O_antiport.
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80.0%;
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GYWLS 100
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P51184;
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MEDLINE=97199138; PubMed=9053381;
Ohtani K., Bando M., Swe T., Banu S., Oe M., Hayashi H., Shimizu T.;
"Collagenase gene (colA) is located in the 3'-flanking region of the perfringolysin O (pfcA) locus in Clostridium perfringens.";
FEMS Microbiol. Lett. 146:155-159(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!- FUNCTION: CATALYZES AN ELECTRONEURAL EXCHANGE BETWEEN ARGININE
AND ORNITHINE TO ALLOW HIGH-ERPICFENCY ENERGY CONVERSION IN THE
ARGININE DEIMINASE BATWAN EN SIMILARITY.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=13 / Type A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium perfringens.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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Pred. No. 1.3e+02;
1; Mismafches 0; Indels
                                                                                                                                Amino-acid transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                    BE91A01F6A2203CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                 EMBL, AJ001330; CAA04686.1; -.
InterPro; IPR002293; AA/rel_prmease1.
InterPro; IPR00481; Permease.
InterPro; IPR004754; R/O_antiport.
Pfan; PF00324; aa_permeases; I.
TIGRFAMs; TIGR00905; 2A0302; I.
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ARCD OR CPE0170.
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80.0%;
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TRANSMEM 10
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94 GYWLS 98
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AC Q46170;
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01-OCT-1996 (Rel. 34, Last sequence update)
115-UNN-2002 (Rel. 41, Last annotation update)
PTS system, sucrose-specific IIBC component (EIIBC-SCR) (Sucrose-permease IIBC component) (Phosphotransferase enzyme II, BC component) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A. STOURT C2A; SEQUENCE PROM N.A. STRAIN-DSM 20267 / Isolate C2A; MEDLINE-94049586; PubMed=8232209; MEDLINE-94040586; PubMed=8232209; MEDLINE-94040586; P., Brueckner R.; Goetz F., Brueckner R.; Caloning and characterization of the scrA gene encoding the sucrose-geocific Enzyme II of the phosphotransferase system from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 1; Length 478;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
Pfam; PF00324; aa permeases; 1.
TIGREAMS: TIGRO0505; 2A0302; 1.
Transport; Antiport; Amino-acid transport; Transmembrane;
Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN REF. 1).
MISSING (IN REF. 1).
A -> V (IN REF. 1).
G -> E (IN REF. 1).
W, A7BA24F7B53A344B CRC64;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1288;
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16-OCT-2001
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P04480;
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
-!- + glycyl-tRNA(Gly).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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15-JUN-2002 (Rel. 41, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS)
GLYS OR APE1639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINET;

MEDLINE-99310339; PubMed=10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,

Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi
Jin-no K., Takahashi M., Mishijima K., Nakazawa H.,

Takamiya M., Masuda S., Punahashi T., Tanaka T., Kudoh Y.,

Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,

"Complete genome sequence of an aerobro hyper-thermophilic

crenarchaeon, Aeropyrum pernix Kl.";
                                                                                                                                                                                                                                                                                                                InterPro; IRR001955; PTS_EIIB.

InterPro; IRR001352; PTS_EIIB.

Refam; PF00379; PTS_EIIB.1.

Refam; PF00379; PTS_EIIB.1.

Refam; PF00379; PTS_EIIB.1.

Reform; PF001379; PTS_EIIB.1.

Reform; PF0010379; PTS_EIIB.1.

Reform; PF0010379; PTS_EIIB.1.

Reform; Refam; PF0010379; PTS_EIIB.2.

Reform; PF0010379; PTS_EIIB.2.

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80.0%; Pred. No. 1.3e+02;
iive 1; Mismatches 0; Indels
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        -!- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
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Best Local Similarity
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MOD_RES
MOD_RES
SEQUENCE
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-!- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING TO DISSIPATION OF CELLULAR ENERGY.

-!- FUNCTION: COLICINS ARE POLYEPETIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.

-!- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morlon J., Lloubes R., Varenne S., Chartier M., Lazdunski C.; "Complete nucleotide sequence of the structural gene for colicin A, a gene translated at non-uniform rate."; J. Mol. Biol. 170:271-285 (1983).
                                                                                                                                                                                                                                                                  PRINTS, PRO1043; TRNASYNTHGLY.
TIGRRAMs; TIGR00389; G1yS dimeric; 1.
PROSITE; PS50862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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Morlon J., Chartier M., Bidaud M., Lazdunski C.;
The complete nucleotide sequence of the colicinogenic plasmid ColA.
The extent of homology with ColE1.";
Mol. Gen. Genet. 211:231-243 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;
"Refined structure of the pore-forming domain of colicin A at 2.4-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1; Length sos
Pred. No. 1.68+02;
Transches 0; Indels
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(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
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                                                             InterPro; IPR002106; AALENA ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_gly.
Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF03129; HGTP_anticodon; 1.
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MEDLINE=84036205; PubMed=6313941;
EMBL; AP000062; BAA80640.1; -.
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-1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92184115; PubMed-1339359; Reymond P., Geourjon C., Roux B., Durand R., Fevre M.; Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from the rumen anaerobic fungus Neocallimastix frontalis: comparison of the amino acid sequence with animals and yeast."; Gene 110:57-63 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                         R PIR; A03504; IXEBCA.

R PIR; A03504; IXEBCA.

R PDB; ICOL; 15-7UE-CA.

R PDB; ICOL; 15-7UE-CA.

R PDB; ICOL; 15-7UE-CA.

R PRO1024; Colicin; 1.

DR PRO1024; CHANICOLICIN.

DR PROSITE; PS00276; CHANINEL_COLICIN; 1.

DR PROSITE; PS00276; CHANINEL_COLICIN; 1.

RM Antiblotic; Bacteriocin; Plasmic; 1.

RM Antiblotic; Bacteriocin; Plasmic; 2010011, 1.

RM Antiblotic; PRO1024; CHANINEL_COLICIN; 1.

RM Antiblotic; PRO1024; CHANINEL_COLICIN; 1.

RM ANTIBLOTIC; PRO1024; PRO1
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Neccallimastix frontalis (Rumen fungus).
Eukaryota: Fungi; Chytridiomycota; Neccallimasticales;
Neccallimasticaceae; Neccallimastix.
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01-AUG-1991 (Rel. 19, Created)
10-AUG-1991 (Rel. 19, Last sequence update)
10-AUN-2002 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
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                                                           EMBL; X01008; CAA25503.1; -. EMBL; M37402; AAA72879.1; -.
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|36 GYWLS 140
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P22130;
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01-MAY-1991 (Rel. 18, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ENV Polyprotein precursor (Contains: Knob protein GP70; Spike protein
PISE].
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PIR; C32595; VCLJGL.
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InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; ENV_polyprotein; 1.
Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.
CHAIN 43 489 KNOB PROTEIN GP70.
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Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
VCBI_TaxID=11840;
                                                                                                                                                                              EMBL, M59372; AAA33553.1; -.

PIR, UQ1462; JQ1462.

R InterPro; IPR000364; PEP_carboxykin.

ProDom; P0004719; PEPCK G.

R PROSITE; PS00505; PEPCK GTP; 1.

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C4D2B249A92B7D26 CRC64;
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Delassus S., Sonigo P., Main-Hobson S.;
"Genetic organization of gibbon ape leukemia virus.";
Virology 173:205-213(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNOB PROTEIN GP70.
SPIKE PROTEIN PISE.
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nes 4; Conserv
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P21415;
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                                                                                                                                                                                                                                          MEDLINE=97420683; PubMed=9276668;
Takai K., Sako Y., Uchida A., Ishida Y.;
Takai K., Sako Y., Uchida A., Ishida Y.;
"Extremely thermostable phosphoenolpyruvate carboxylase from an extreme thermophile, Rhodothermus obamensis.";
J. Blochem. 122:32-40(1997).
-!- FUNCTION: TO FORM OXALOACTATE, A FOUR-CARBON DICARBOXYLIC ACID SOURCE FOR THE TRICABBOXYLIC ACID CYCLE. THE OPTIMUM TEMPERATURE FOR ACTIVITY IS 75 DEGREES CELSIUS. THE ENZYME EXHIBITS A PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pi35I1; P94142;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cobalt-zinc-cadmium resistance protein czcA (Cation efflux system
                                                                Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) (PEPC) PPC OR PEPC.
                                                                                                                          Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Crenotrichaceae; Rhodothermus.
NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
Ralstonia.
NCBI_TaxID=510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.9%; Score 30; DB 1; Length 936; 80.0%; Pred. No. 2.5e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                OPTIMUM OF 8.0. CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
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RE 155 155 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoenolpyruvate + CO(2).
-! CORACTOR: ABSOLUTE REQUIREMENT FOR DIVALENT CATIONS.
-!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBUNIT: HOMOTETRAMER.
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107886 MW; C9AA94C3F26C345A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                          Rhodothermus marinus (Rhodothermus obamensis)
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PROSITE; PS00393; PEPCASE 2; 1.
PROSITE; PS00781; PEPCASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001449; PEPcase.
Pfam; PF00311; PEPcase; 1.
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HSSP; P00864; 1FIY.
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GYWMA 602
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              01-NOV-1997
01-NOV-1997
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ACT SITE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase)
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Pfam; PF03648; Glyco hydro 67; 1.
Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
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0
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"The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                        Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
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                                90.9%; Score 30; DB 1; Length 667;
80.0%; Pred. No. 1.8e+02;
iive 1; Mismatches 0; Indels
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. ~ 0; Indels
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73729 MW; SFFB32F00D8631BE CRC64;
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ALPHA-GLACURONIDASE.
N-LINKED (GLCNAC.
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STRAIN=QM9414 / Rut C-30;
MEDLINE=96257277; PubMed=8654984;
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                                                                          4; Conservative
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767 7
847 AA;
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180 GYWLS 184
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                                                STRAIN=CH34;
MEDLINE=90017477; PubMed=2678100;
Nies D.H., Nies A., Chu L., Sllver S.;
MEXpression and nucleotide sequence of a plasmid-determined divalent cation efflux system from Alcaligenes eutrophus.";
Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355(1989).
                                                                                                                                                                                                                                                                                  InterPro: IPR001036; Acrflvin_res.
InterPro: IPR004763; CzcA.
InterPro: IPR004763; ACR tran; InterPro: InterPro: InterPro: IPR00476; ACR tran; InterPro: Int
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115668 MW; 1E95B7923996AEBC CRC64;
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STRAIN=CH34;
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Matches
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Search completed: April 22, 2003, 12:51:50 Job time : 4.5 secs

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                                                     April 22, 2003, 12:47:43; Search time 10 Seconds (without alignments) 103.024 Million cell updates/sec
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                    protein search, using sw model
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ALIGNMENTS

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MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MG W.V., Kennedy S.R., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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100.0%; Score 33; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          VNG2253H.
Halobacterium sp. (strain NRC-1).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceee; Halobacterium.
NCBI_TaxID=64091;
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SEQUENCE 67 AA; 6601 MW; A6BAF23FCBE8B648 CRC64;
                                                                   01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                 67 AA
                               PRT;
                                   PRELIMINARY;
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Q9HN48;
RESULT 1
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368 GYWMS 372
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MEDLINE-20115608; PubMed=10648209;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Molecular systematics of the African electric fishes (Morwyroidea: Wolecular systematics of the evolution of their electric organs.";

J. Exp. Biol. 203:665-683 (2000).

Exp. Biol. 203:665-683 (2000).

EMBL, AF201625; AAF43336.1; -.

InterPro; IRR004331; RAG2.

Ffam, PP03089; RAG2; 1.

NON TER 17 377

SEQÜENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;
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SEQUENCE FROM N.A.

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

"Molecular systematics of the African electric fishes (Mormyroidea:

"Molecular systematics of the African electric organs.";

Teleostei) and a model for the evolution of their electric organs.";

D. Exp. Babl., 203:665-683 (2000).

EMBL, AF201616; AAF43327.1;

InterPro; IPR004321; RAG2.

NON TER 377 377
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Bullengeromyrus knoepfileri.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Boulengeromyrus.
                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygli, Neopterygli, Teleostel, Osteoglossomorpha, Osteoglossiformes, Mormyridae; Campylomormyrus.
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                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Campylomormyrus tamandua.
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Sullivan J.P., Lavoue S., Hopkins C.D.;
"Molecular systematics of the African electric fishes (Mormyroidea:
"Molecular systematics of the African electric fishes (Mormyroidea:
"Molecular systematics of the African electric fishes (Mormyroidea:
"Teleostel) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000).
EMBL; AF201619; AAF43330.1; -.
Pitan: PF03089; RAG2: 1.

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SEQÜENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;
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EMBL, AFDG168; AR43329.1; -.

Ffam; PF03089; RAG2; 1.

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SEQÜENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2001 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment)
Brienomyrus hopkinsi
Eukaryota; Mecazaa; Chardata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
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Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopteroryi; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
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llarity 100.0%; Pred. No. 2.2e+02;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
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les 5; Conserv
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RESULT

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### STATE | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 
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MEDLINE-20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
"Molecular systematics of the African electric fishes (Mormyroidea: Telecotei) and a model for the evolution of their electric organs.";
Telecotei) and a model for the evolution of their electric organs.";
Telecotei) and a model for the evolution of their electric organs.";
EMBL; AF201623; AAF43334.1;
InterPro; IPR004321; RAG2.
Pfam; PF03089; RAG2; 1.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Campylomormyrus sp. 1P81-2000.
Shraryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Mormyridae; Campylomormyrus.
                                             01-007-2000 (TrEWBLrel. 15, Created)
01-007-2000 (TrEWBLrel. 15, Last sequence update)
01-007-2000 (TrEWBLrel. 15, Last sequence update)
Recombination-activating protein 2 (Fragment).
Campylomormyrus numenius.
Bararyota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostel; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Campylomormyrus.
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100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels 0
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100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
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377 Aa; 41357 MW; DDA7ED06162C799A CRC64;
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377 AA
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   PRELIMINARY;
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Q9IAG7
ID Q9IAG
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Q9IAG9
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MEDIJIRE-20115608; PubMed=10648209;
MEDIJIRE-20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
"Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000)
EMBL; AF201621; AAF43332.1;
InterPro; IRR004421; RAG2.
Pfam; PF03089; RAG2.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Brienomyrus sp. CU79740.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
                                                                                                                                                                                                                                     Bukaryori, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha, Osteoglossiformes, Mormyridae, Brienomyrus.
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377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;
                                                            091AH2;
01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last amnotation update)
Recombination-activating protein 2 (Fragment).
Brienomyrus niger.
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                                       377 AA
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100...
Best 5; Conservative
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368 GYWMS 372
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Sullivan J.P., Lavoue S., Hopkins C.D.;
"Moldecular systematics of the African electric fishes (Mormyroidea:
"Moldecular systematics of the African electric fishes (Mormyroidea:
"Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:65-683(2000).
EMBL, AF201630; AR43341.1;
"InterPro; IPR004321; RAG2.
PÉAM; PF03089; RAG2; 1.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Hippopotamyrus discorhynchus (Zambezi parrotfish).
Bukaryota, Metazoa, Chordata, Craniata, Vartebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Hippopotamyrus.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=20115608; PubMed=10648209;
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Q9IAG2
ID Q9IAG2
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   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Geomyomyrus donnyi.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Osteoglossiforms; Mormyridae; Genyomyrus.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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Matches 5; Conservative
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Q91AG4;
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MEDLINE=20115608; PubMed=10648209;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Teleostei) and a model for the Arrican electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";

J. Exp. Biol. 203:665-683 (2000).

InterPro; IPRO04321; RAG2.

InterPro; IPRO04321; RAG2.

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NON_TER 377 377

SEQÜENCE 377 AA; 41491 MW; IBE26037590CA937 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Hippopotamyrus pictus.
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli; Neopterygli; Teleostel; Osteoglossiformes; Mormyridae; Hippopotamyrus.
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                                                                                                  ; Score 33; DB 13; Length 377;
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NON TER 1 1
NON TER 377 377
SEQUENCE 377 AA, 41293 MW, 9F7C51AF89B736C4 CRC64;
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Q91AG2;
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Sullivan J.P., Layoue S., Hopking C.D.;
Sullivan J.P., Layoue S., Hopking C.D.;
Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the african electric organs.";
J. Exp. Biol. 203:665-683(2000).
BMBL; AP201633; AAR43344.1; -.
InterPro; IPR004321; RAG2.
Fam; PF03089; RAG2; 1.
NON TER 1
NON TER 377 377
SEQÜENCE 377 AA; 41324 MW; C3C5A2BBE34EF6FC CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hippopotamyrus wilverthi.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
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Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Hyperopisus.
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100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last ann
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Search completed: April 22, 2003, 12:53:50 Job time : 11 secs

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April 22, 2003, 12:45:19 ; Search time 12.6786 Seconds (without alignments) 52.550 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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1: /SIDS2/gcgdata/
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Maximum DB seq length: 2000000000
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33
1 GYWMS 5
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                                                                                                                                                                                                                                                                                               OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Light chain CDR H1	Mouse anti-CD23 MA	Humanised anti-CD2	Drosophila melanog	Novel human diagno	V39, monoclonal an	Human secreted pro	Chlamydia pneumoni	Novel signal trans	Rat HT glycoprotei
SUMMARIES		ID			AAY32260	AAY32263	ABB62006	ABG07533	AAR95472	AAY07813	AAY35482	AAU17327	AAY76114
		80	1111	21	21	21	22	22	17	20	20	22	21
	Query e Match Length DB I	1	ហ	137	444	1254	40	43	64	181	210	242	
	æ	Query Match	1 1 1 1 1 1	100.0	100.0	100.0	100.0	6.06	90.9	90.9	90.9	90.9	90.9
		Score		33	33	33	33	30	30	30	30	30	30
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(GLAX) GLAXO GROUP LTD.

Skin cell protein, Rat protein isolat Rat protein isolat Rat protein isolat Staphylococcus epi Enterococcus faeca		Human secreted pro Amino acid sequenc EGF-like homologue Human PRO214 prote Human polypeptide	PRO214 pol 4. Homo sa PRO214 pro TANGO 206 TANGO 206 TANGO 206	•	Human angiogenesis Human PRO214 prote Human PRO protein, Streptococcus pneu Streptococcus pneu
233332	22222		420 22 AAB68594 420 22 AAB68594 420 22 AAB80230 420 22 AAB48106 420 22 AAB48110 420 22 AAB48133	22 AAB4813 22 AAB4813 22 AAB4813 22 AAB4813 22 AAB4813 22 AAB4813	420 23 ABB95431 420 23 ABB84825 420 23 AAU33652 448 22 AAU37919 449 21 AAY81542 451 23 ABP25669
		0,0,0,0,0			900.00
11 12 13 14 15 16	11 11 20 21	2 5 5 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	, 3 3 3 5 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	. ഷ സ സ സ സ 4 സ ശ ഗ യ ഗ	6 4444444 10112842

ALIGNMENTS

CD23; PCERII; IgB receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoco's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; uurticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn; s disease; s)ogran's syndrome; allergy, asthma; rhinitis; eczema; insulitis; graft.versus-host disease; COPD; bronchitis; diabetes; Light chain CDR H1 of mouse anti-CD23 MAb C11. AAY32257 standard; Peptide; 5 AA. 99WO-GB01434. 98GB-0009839 B-cell malignancy; therapy 15-FEB-2000 (first entry) WO9958679-A1 07-MAY-1999; 09-MAY-1998; Mus musculus 18-NOV-1999. AAY32257; N

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59 GYWMS 63
                        07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYWMS 5
                                                 09-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                     This sequence represents complementarity determinating region 1 (CDR HI) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32253). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise utficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to render them_repable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematous, Hashimoto's thyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogran's syndrome, allergies, allergic asthma, intrinsic asthma, acte asthma, acte asthma, care asthma, care asthma, disease, COPD, insulitis, bronchitis cacema, graft-versus-host disease, COPD, insulitis, bronchitis diabetes), and B-cell malignancies (claimed). They are also useful for etermining the binding agents.
                                                          Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; porlasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; aethma; rhinitis; eczema; insulitis; graff.-vergus-host disease; COPD; bronchitis; diabetes;
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Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 33; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse anti-CD23 MAb Cll heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY32260 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CDR H1"
78..96
/note= "CDR H2"
129..131
/note= "CDR H3"
                                                                                                Claim 1; Page 40; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 5; Conservative
                       WPI; 2000-053101/04.
                                   N-PSDB; AAZ34742
                                                                                                                                                                                                                                                                                                                                                                  5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYWMS 5
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                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32260;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY32260
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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody Cl1. The invention provides altered antibodies, such as chimeric or humanised antibodies less AAV32262 and AAV32263), which comprises sufficient of antibodies (see AAV32262), which comprises sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions (see AAV32254-59) for render them capable of binding to the CD23 type II molecule expressed on hamman therapy, for the treatment of arthritis, lammatopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimto's thyroiditis, multiple sclerosis, labered verthematosus, Hashimto's thyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, psoriasis, uriticalis, actualitis, inflammatory bowel disease, ulcerative colitis, crohn's disease, sinflammatory bowel disease, ulcerative colitis, troin's disease, Signers asthmatic excension; rhinitis, contine, acute asthmatic excension; rhinitis, excension; diabetes (particularly type I (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful cetermining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Pred. No. 69;
                                                                                                                                                                                                                                                            Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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99WO-GB01434.
                                                                                       98GB-0009839.
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                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
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N-PSDB; AAZ34745.
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(first entry)

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                      Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.
                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 12810.
ABB62006 standard; Protein; 1254 AA
                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
N-PSDB; ABL06109.
                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                 WO200171042-A2
                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                   27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGRVII) and the heavy chain complementarity determining regions (see AAV32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides attered antibodies, such as chimanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematorous, Hashimoto's thyroiditis, multiple sclerosis, clabeles, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulomephritis, inflammatory bowel disease, ulcerative collitis, crohn's disease, Sjogrem's syndrome, allergies, allergic athma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchiis (particularly thronic bronchiis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful contents of the substances (claimed) and second contents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rapson NT,
                                                                                                                                                                                                                                              /note= "framework region 4"
112..444
/note= "constant region"
                                note= "framework region 1"
                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crowe SJ, Ellis JH,
ocation/Qualifiers
                                                                                                                                             /noc.
69..100
' ---= "framework r
                                                                                     36..49
/note= "framework r
50..68
/note= "CDR 2"
                                                                                                                                                                              /noce-
101..103
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                                                                    "CDR 1"
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                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB01434.
                                                                                                                                                                                                                                                                                                                                                                                                                              98GB-0009839
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                                                                                                                                                                                                                                 104..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROUP LID.
                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-053101/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
                                                                                                                                                                                                                                                                                                                      W09958679-A1
                                                                                                                                                                                                                                                                                                                                                          18-NOV-1999.
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Key
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Matches
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Myers EW;

Li PWD,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511),
                                                                                                                                                                        (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                      Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                 h similarity 100.0%; Score 33; DB 22; Similarity 100.0%; Pred. No. 6.6e+02; 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #7524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG07533 standard; Protein; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                    1254 AA;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1139 GYWMS 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                         Sequence
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RESULT 4 ABB62006

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us-09-674-716b-9.open.rag

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Human, secreted protein, prevention, treatment, protein therapy, gene therapy, diagnosis, cancer; tumour; neurodegenerative disorder; gene therapy, diagnosis, cancer; tumour; neurodegenerative disorder; lymphoma; developmental abnormality, foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma, sepais; diabetes; AIDS; Altheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR95459-R95509 are antigen binding peptides ("abtides") derived from the monoclonal antibody SM-3 which recogniese a specific polymorphic epithelial mucin tumour antigen found on human breast cancer cells. The abtides are identified from random peptide libraries using specific ligand binding. Abtides mimic the binding specificity of smaller size allowing their production at a lower cost and reducing the extent of their immunogenicity aiding in vivo delivery. The abtides are useful for the diagnosis, detection, imaging and treatment of disease, e.g. tumours, prostate cancer and breast
                                                                                                                                                                                                                                                                                                                New isolated peptide(s) with specific binding activities - obtd. by screening random peptide libraries, for use in diagnostic and therapeutic compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.9%; Score 30; DB 17; Length 43; 80.0%; Pred. No. 77; 1.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein fragment encoded from gene 70.
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 38; Page 75; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY07813 standard; Protein; 64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0092956.
98US-0092956.
97US-0056368.
97US-0056369.
                                                              95WO-US11934.
                                                                                                           95US-0488161.
94US-0310192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.v.
A; Conservative
                                                                                                                                                                                 (CYTO-) CYTOGEN CORP
                                                                                                                                                                                                                                                                        WPI; 1996-188471/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GYWLS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9909155-A1.
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15-JUL-1998;
19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                20-SEP-1995;
                                                                                                           07-JUN-1995;
21-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999.
                      28-MAR-1996
                                                                                                                                                                                                                              Alvarez VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY07813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer.
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (I) be useful as hybridisation probes, polypeptide (II) sequences. (I) brimers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymocleotides are also used in disgnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to tread disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Condet amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V39, monoclonal antibody SM-3 derived antigen binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 22; Length 40;
Pred. No. 71;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 37892; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR95472 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.94;
                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS71720.
                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 AA;
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 GYWLS 37
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                                          11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR95472;
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Neuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anemia! hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alaheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; acardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                     AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.9%; Score 30; DB 20; Length 181; 80.0%; Pred. No. 3.3e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel signal transduction pathway protein, Seg ID 892.
                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                   Page 1244; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU17327 standard; Protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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                                                                 98US-0107078.
97FR-0014673.
                          98WO-IB01890
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                                                                                                                                                                                                                WPI; 1999-357842/30.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AA;
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                                                                                                                             (GEST ) GENSET
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04-FEB-2000; 2
24-FEB-2000; 2
02-MAR-2000; 2
16-MAR-2000; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWMS 5
                          20-NOV-1998;
                                                                                       21-NOV-1997;
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                                                                                                                                                                        Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:|
48 GYWLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides. Specific uses are the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune (alsorders, leukemias, disease, lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzhaimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine disorders, infections and ALDS. The human secreted proteins of the invention are represented in AAX37369-X37441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                                                                           Soppet DR;
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80.0%; Pred. No. 1.2e+02;
7ative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                Feng P;
Lafleur I
Shi Y, S
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                                                                                                                                                                                                              A, Duan R, Ebner R, Endress GA, C, Florence KA, Komatsoulis GA, Olsen HS, Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1b; Page 264; 280pp; English.
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97US-0056535.
97US-0056555.
97US-0056556.
97US-0056528.
97US-0056728.
                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX37438.
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                                                                                                         19-AUG-1997;
    19-AUG-1997
                        19-AUG-1997
                                                                 19-AUG-1997
                                                                                     19-AUG-1997
                                                                                                                                                                                                                                  Florence C,
Moore PA,
Young PE;
                                                                                                                                                                                                                  Brewer LA,
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Sequence

%XXCCCCCCCCCCCXXXXTTTXXXXXIIIIII

Query Match Matches

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RESULT 8 AAY35482

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                                               2000US-0205515.
2000US-0215135.
2000US-0215135.
2000US-0216800.
2000US-0216800.
2000US-0216800.
2000US-0216800.
2000US-0225213.
2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225266.
2000US-0225266.
2000US-0225266.
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2000US-0225266.
2000US-0225268.
2000US-022528.
2000US-022528.
2000US-022528.
2000US-022528.
2000US-022928.
2000US-022928.
2000US-0231244.
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2000US-0231368.
2000US-0231368.
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2000US-0235484.
2000US-0235334.
2000US-0235334.
2000US-023535.
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19-SEP-2000

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02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
117-MAR-2000;

18-AYR-2000;

28-JUN-2000;

28-JUN-2000;

07-JUN-2000;

07-JUN-2000;

07-JUL-2000;

11-JUL-2000;

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13-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0240960.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-024617.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246521.
08-NOV-2000; 2000US-0249211.
08-NOV-2000; 2000 2000US-0251030. 2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0251856. 2000US-0251868. 2000US-0254097 2001US-0259678 17-NOV-2000, 2 01-DBC-2000, 2 05-DBC-2000, 2 05-DBC-2000, 2 06-DBC-2000, 2 06-DBC-2000, 2 08-DBC-2000, 2

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-465460/50. N-PSDB; AAS27244.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 892; 880pp; English

and The invention relates to novel isolated polypeptides (I),

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polynucleotides (II). (I) (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune tisorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and cher blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haemotopoietic disorders, hyperproliferative disorders, primary haemotopoietic disorders, hyperproliferative disorders (e.g. danaemia), myeloproliferative disorders (e.g. danaemia), myeloproliferative disorders (e.g. danaemia), respiratory disorders, dermacological disorders (e.g. arnythmia), respiratory disorders, dermacological disorders, in wound healing, epithelial cell proliferation, endocrine disorders, in wound healing, epithelial cell proliferation, endocrine disorders, can disorder (inflammatory disorders), liver disorders (erg. T-cells, to induce higher affinity antibodies, and as means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AlbS). AAU1705-AAU17083 represent novel signal transduction control setting amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; disease; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides useful for the treatment of various conditions
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Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat HT glycoprotein homologue, SEQ ID NO:393.
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98US-0188930.
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Best Local Similarity 80.0%;
Matches 4; Conservative
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68 GYWLS 72
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The invention relates to novel nucleic acid sequences derived from rat

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dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to transit inflamation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences ANT5942-Y76121 represent polypeptides encoded by the NATS942-Y76121 represent polypeptides encoded by the NATS942-Y7613 represent polypeptides encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murison JG;
                                                                                                                                                                                          by CDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY761122 are proteins with one or more putative transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                          Length 242;
                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 21; Length 24
Pred. No. 4.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onrust R, Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 297-298; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB56053 standard; Protein; 242 AA.
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                                                                                                                                                                                                                                                                                                                                                                              90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-007495/01.
N-PSDB; AAC99755.
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          242 AA;
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224 GYWLS 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWMS 5
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                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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ABB72290 standard; Protein; 242 AA.
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                                                              ABB72290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of CDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammarcory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kumble KD;
                                                                                                                                                                                                                                                                                                    Human; rat; mouse; skin cell; skin wownd; cancer; growth defect;
developmental defect; inflammatory disease; dermatological; vulnerary;
immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynuclectides and polypeptides encoded by the polynuclectides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
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                                                                     DB 22; Length 242;
4.4e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.9%; Score 30; DB 23; Length 242;
80.0%; Pred. No. 4.4e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Rat protein isolated from skin cells SEQ ID NO: 393.
                                                                        Score 30; DB
Pred. No. 4.4e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                       ABB72253 standard; Protein; 242 AA
                                                                       Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulating immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2001; 2001WO-NZ00099
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-122020/16.
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Matches 4; Conserv
                                                 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA;
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                                                                                                                                                                                                                                                                                                                                                   Rattus sp
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                                                  Sequence
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The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumble KD;
                                                 Human, rat, mouse, skin cell, skin wound; cancer, growth defect, developmental defect, inflammatory disease, dermatological, vulnerary; immunomodulator, anti-inflammatory, cytostatic; neuroprotective.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
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80.0%; Pred. No. 4.4e+02;
ive 1; Mismatches 0; Indels
Rat protein isolated from skin cells SEQ ID NO: 502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleeman M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 308; 466pp; English.
                                                                                                                                                                                                                                                                                                                           24-MAY-2001; 2001WO-NZ00099.
                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulating immune responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-122020/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AA
                                                                                                                                                                                                                WO200190357-A1.
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224 GYWLS 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watson JD,
                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB72301;
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224 GYWLS 228

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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4114.
                                                                                                                                                                                                                                                                                                            ABP39269 standard; Protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                               97US-055779P
97US-064964P
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0134001
                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                    Conservative
                                                                                      Strachan L,
                                                                                                 WPI; 2002-122020/16.
N-PSDB; ABL34986.
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                            242 AA;
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224 GYWLS 228
                  WO200190357-A1.
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                     24-JUL-2002
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                               29-NOV-2001
                                                                                      Watson JD,
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ABP39269
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                     Novel isolated nucleic acid encoding a Staphylococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                   Disclosure; SEQ ID 4114; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 22, 2003, 12:51:15 Job time : 14.6786 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.9%;
Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                WPI; 2002-381255/41.
N-PSDB; ABN91814.
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Matches 4; Conserv
Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USPTO web site.
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52 GYWLS 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of CDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                 Kumble KD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
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                                                                                                                                                                                                                                                                                                                                                                    Murison JG,
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                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulating immune responses
                                                                                                                                                                                                                                      24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
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Gaps

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Score 30; DB 23; Length 243; Pred. No. 4.5e+02; 1; Mismatches 0; Indels

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Gaps
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Sequence 109,
Sequence 109,
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Sequence 290,
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Sequence 122,
Sequence 109,
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Sequence 122,
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                    Sequence
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; Sequence 892, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 64;
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US-09-906-838-109
US-09-907-613-109
US-09-907-613-109
US-10-176-918-290
US-10-176-918-290
US-10-176-918-290
US-10-176-918-290
US-10-137-865-290
US-10-137-865-290
US-10-140-474-290
US-09-904-820-109
US-09-904-820-109
US-09-904-786-109
US-09-903-7494-109
US-09-903-7494-109
US-09-903-7494-102
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; OTHER INFORMATION: Xaa equals stop translation
US-10-144-929-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 9; Pred. No. 69; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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80.0%;
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Best Local Similarity 80.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
        |||:|
GYWLS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-764-868-892
          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 393, A
Sequence 502, A
Sequence 625, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     April 22, 2003, 12:53:59 ; Search time 5.26786 Seconds (without alignments) 76.055 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-144-929-162
US-09-764-868-892
US-09-866-050A-502
US-09-866-050A-625
US-09-815-242-10910
US-10-650-704-10910
US-10-144-929-156
US-09-907-824-109
US-09-906-742-290
US-10-121-049-290
US-10-121-049-290
US-10-121-049-290
US-10-121-049-290
                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 301932 seqs, 80129803 residues
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                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                             OM protein
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; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watenon, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Steeman, Matthew
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REPRENCE: 11000.1011c4U
; CURRENT APPLICATION UNDER: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SEQ ID NO 625
; SEQ ID NO 625
; LEMTH: 242
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Patent NO. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haaelbeck, Robert
APPLICANT: Carri Carnit Carri Carri Carnit Carri Carri Carnit Carri Carnit Carri Carnit Carri Carnit Carri Carnit Carri Carnit C
                                                                                                                                                                        Length 242;
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80.0%; Pred. No. 2.3e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                 Score 30; DB 9; Length 242
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                 Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 4; Conserv
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US-09-815-242-10910
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US-09-866-050A-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-866-050A-625
                                                                        ; ORGANISM: Rat
US-09-866-050A-502
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             LENGTH: 242
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; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 892
ILENGTH: 210
; TYPE: PRT
; CREANISM: Homo sapiens
US-09-764-868-892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 393, Application US/09866050A
; Sequence 393, Application US/09866050A
; Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, James G.
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
ITILE OF INVENTION: Compositions Isolated From Skin Cells
ITILE OF INVENTION: Compositions of Their Use
ITILE OF INVENTION: Compositions of Their Use
ITILE OF INVENTION: And Methods for Their Use
ITILE OF INVENTION: And Methods for Their Use
ITILE REFERENCE: 1000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; GURRENT FILING DATE: 2001-05-24
; NUMBER: PSESTSEQ for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4

US-09-866-050A-502

i Sequence 502, Application US/09866050A

j Publication No. US20030040471A1

i GENERAL INFORMATION:

i APPLICANT: Strachan, Lorna

j APPLICANT: Strachan, Lorna

j APPLICANT: Sleeman, Matthew

APPLICANT: Murison, James G.

i APPLICANT: Murison, James G.

j APPLICANT: Murison, James G.

i TITLE OF INVENTION: Compositions Isolated From Skin Cells

i TITLE OF INVENTION: and Methods for Their Use

i FILE REFERENCE: 11000.1011c4U

CURRENT FILING DATE: 2001-05-24

i NUMNER OF SEQ ID NOS: 725

i SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.9%; Score 30; DB 9; Length 210; Best Local Similarity 80.0%; Pred. No. 25+02; Matches 4; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0,
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224 GYWLS 228
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68 GYWLS 72
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US-09-866-050A-393
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ORGANISM: Rat
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374 GYWLS 378
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US-09-905-291A-109
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APPLICANT:
APPLICANT:
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, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-050-704-180
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US-10-144-929-156
Sequence 156, Application US/10144929
Publication No. US20030069405A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFRENCE: PZ014P1
CURRENT APPLICATION NUMBER: US/10/144,929
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/251,329
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US-10-050-704-180

is aguence 180, Application US/10050704

publication No. US20030050442A1

igenbrah. INFORMATION:

igenbrah. INFORMATE:

igenbrah
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10910
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10910
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87 GYWLS 91
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LENGTH: 392
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PRIOR FILMO NUMBER: PC7-1798/17044

PRIOR FILMO PRINT 1999-00-18

NUMBER OF SELINO NUMBER: PC7-1798/17044

NUMBER OF SELINO NO. 275-00-18

SOCTAME: Patentin Ver. 2.0

SOCTAME: Patentin Ver. 2.0

SOCTAME: Patentin Ver. 2.0

SOCTAME: Patentin Ver. 3.0

GOGNAME: Patentin Ver. 3.0

APPLICAN: Patentin Ver. 3.0

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Pred. No. 3.9e+02;
1; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2854
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-07
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Goo, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Botstein, David
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Eaton, Dan L.
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US-09-902-853-109
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
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                                                            PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-09
PRIOR PELLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28114
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1909-12-20
PRIOR PILING DATE: 1909-12-20
PRIOR PILING DATE: 1909-12-20
PRIOR PILING DATE: 1909-12-20
PRIOR PILING DATE: 2000-01-05
                                          FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
            APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
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Publication No. US20020192659A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botetein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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US-09-905-291A-109
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US-09-902-853-109
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APPLICANT:
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Gaps

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APPLICANT: Tumas, Daniel
APPLICANT: William, P. Wickey
APPLICANT: William, P. Wickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT FILING DATE: 2001-11-20
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: DCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-09-04
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-
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APPLICANT: Genentech, Inc.; APPLICANT: Botstein, David; APPLICANT: Besnoyers, Luc; APPLICANT: Eaton, Dan L. APPLICANT: Ferrara, Napoleone; APPLICANT: Ferrara, Napoleone; APPLICANT: Filvaroff, Ellen
                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                               Gerber, Hanspeter
                                                                                                                Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                Kljavin, Ivar J.
Mather, Jennie P.
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           ong, Sherman
ao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/907,824 CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                    PRIOR PELICATION NUMBER: 09/665,350
PRIOR PELIANG DATE: 2000-09-18
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PRIOR PELIANG DATE: 2000-02-22
PRIOR PELIANG DATE: 1000-02-22
PRIOR PELIANG DATE: 1090-07-07
PRIOR PELIANG DATE: 1999-07-05
PRIOR PELIANG DATE: 1999-07-26
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PRIOR PELIANG DATE: 1999-11-30
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PRIOR PELIANG DATE: 1999-12-02
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PRIOR PELIANG DATE: 1999-12-02
PRIOR PELIANG DATE: 1999-12-02
PRIOR PELIANG DATE: 1999-12-02
PRIOR PELIANG DATE: 1999-12-03
PRIOR PELIANG DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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US-09-907-824-109
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Best Local Similarity
Matches 4; Conserv
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RESULT 14
US-10-028-072-290
IS-10-028-072-290
Septime 290, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                   Sherwood, Steven
Smith, Victoria
Stewart, Timothy
                                                                                                                                                                                                                              Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Danie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
                                                                                        LICANT: Gir...
LICANT: Gir...
LICANT: Gir...
LICANT: Gir...
LICANT: Mather. James I.
PLICANT: Paril Mitchlas F.
PLICANT: Stewart. Timechy A.
PLICANT: Stewart. Timechy A.
PLICANT: Gir...
PRICANT: Gir...
PRICANT: MATHER, DATE: James I.
LITLE OF THYMENION: Acid Encoding the Same
CURRENT PAPLICATION NUMBER: 105/06/04.011
CURRENT PAPLICATION NUMBER: 09/065.350
FRIOR PAPLICATION NUMBER: 09/06.04414
FRIOR PAPLICATION NUMBER: 09/06/04/414
FRIOR PAPLICATION NUMBER: 09/06/04/414
FRIOR PAPLICATION NUMBER: 09/07/08/04/414
FRIOR PAPLICATION NUMBER: 10/06/04/414
FRIOR PAPLICATION NUMBER: 10/06/04/414
FRIOR PAPLICATION NUMBER: 10/06/04/414
FRIOR PAPLICATION NUMBER: 10/06/04/46
FRIOR PAPLICATION NUMBER: 10/06/06/46
FRIOR PAPLICATION NUMBER: 10/06/06/46/46
FRIOR PAPLICATION NUMBER: 10/06/06/46/46
FRIOR PAPLICATION NUMBER: 10
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                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
        Gerber, Hanspeter
Gerritsen, Mary E
                                APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT PELING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 05/049911
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PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-26
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PRIOR PLING DATE: 1997-10-27

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PRIOR FILING DATE: 1997-10-28

PRIOR PAPLICATION NUMBER: 60/063735

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PRIOR APPLICATION NUMBER: 60/063735

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PRIOR PELING DATE: 1997-12-11

PRIOR PLING DATE: 1998-02-09

PRIOR PLING DATE: 1998-03-25

PRIOR PLING DATE: 1998-04-19

PRIOR PLING DATE
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Gaps

RESULT 15
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US-09-906-742-109
; Sequence 109, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:

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APPLICANT: Generate, Inc.
APPLICANT: Galester, Javid
APPLICANT: Batherat, Avid
APPLICANT: Betsoyer, Luc
APPLICANT: Plivarcff Ellien
APPLICANT: Plivarcff Ellien
APPLICANT: Gao, Wei-Ciang
APPLICANT: Garmalli, Critetopher J.
APPLICANT: Manager, Jamie P.
APPLICANT: Manager, Jamie P.
APPLICANT: Manager, Jamie P.
APPLICANT: Roy, Managered and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INPARTICANT NUMBER: 1999-07-16/143-049
PRIOR PLILIKO DATE: 1999-07-16/143-049
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PRIOR PLILIKO DATE: 1999-07-18 FOUNDS-07-18
PRIOR PLILIKO DATE: 1999-07-18 FOUNDS-07-18
PRIOR PLILIKO DATE: 1999-07-18
PRIOR PLILIKO DATE: 1999-11-17
PRIOR PLILIKO
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 402 GYWLS 406
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Job time: 6,26786 secs
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Sequence 414, Appl
Sequence 5, Appli
Sequence 22, Appli
Sequence 21, Appl
Sequence 31, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appli
Sequence 3, Appli
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Sequence 39, Appl
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                                                                                                                                          April 22, 2003, 12:48:49; Search time 4.375 Seconds (without alignments) 33.626 Million cell updates/sec
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                        GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-273-685-39
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US-09-134-001C-4114
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US-08-68-451B-31
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US-08-63-451B-19
US-08-05-434-18
US-08-05-434-19
US-08-05-44-65-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
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1 GYWMS 5
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Match Length DB
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Perfect score:
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                                                                                                       OM protein
                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                              Run on:
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No.
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       Gaps
   23,
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1 Sequence 39, Application US/08489161

Patent No. 5885577

2 **CRIBERAL INFORMATION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS: 103

CORRESPONDENCE ADDRESS: Abonue of the Americas STREET: 1155 Avenue of the Americas CITY: New York

COUNTRY: USA

ZIP: 10036

COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: O'-1UN-1995

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

MAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872

REBERENCE/COMPUTION: THORMATION:

MAME: Mistock, S. Leslie

REGISTRATION NUMBER: 1101-176

TELECOMMUTICATION NUMBER: 1101-176

TELECOMMUTICATION NUMBER: 1101-176

TELECOMMUTICATION INFORMATION:

TELECOMMUTICATION NUMBER: 1101-176

TELECOMMUTICATION NUMBER: 1101-176

TELECOMMUTICATION NUMBER: 120-9741/8864
                                                                       Sequence Seq
                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
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Sequence
Sequence
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US-08-318-1578-23
US-08-053-45518-32
US-08-25-5348-19
US-07-942-245-37
US-08-244-626-10
US-07-942-246-10
US-07-942-246-17
US-09-376-330-20
US-09-376-330-20
US-09-355-8038-95
PCT-US93-09166-3
US-08-318-1578-9
US-08-318-1578-9
US-08-318-1578-9
US-08-318-1578-9
US-08-318-1578-9
US-08-318-1578-10
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US-08-318-1578-10
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-9741/8864
TELEX: 6644 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.98;
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Best Local Similarity 80.0°
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us-09-674-716b-9.op n.rai

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Sequence 4114, Application US/09134001C

| Sequence 4114, Application US/09134001C
| Sequence 4114, Application US/09134001C
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCUS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
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| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION TOWARD FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF TITLE TOWARD FOR PROPERTY FOR THE
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APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 5; Length 43; Pred. No. 45; 0; Indels 1; Mismatches 0; Indels
                                           CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Lealie

REGISTRATION NUMBER: 1101-196-228

TELECOMMUNICATION NUMBER: 1101-196-228

TELERNER/DOCKET NUMBER: 1101-196-228

TELERNER/DOCKET NUMBER: 1790-9090

TELERNER/CATION INFORMATION:

TELERNER/CATION INFORMATION:

TELERNER/CATION INFORMATION:

TELERNER/CATION INFORMATION:

TELERNER/CATION INFORMATION:

TELERNER/CATION FOR SEQ 1D NO: 39:

SEQUENCE CHARACTER/STICS:

LENGTH: 43 amino acids
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                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-005-315-127-5
; Sequence 5, Application US/09315127
; Patent No. 6448390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide PCT-US95-11934-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-09-134-001C-4114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GYWLS 10
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; Sequence 39, Application PC/TUS9511934
; GeneRAL INFORMATION:
; APPLICANT: Cyclen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 3; Length 43;
Pred. No. 45;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZUCHALLY 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PattentIn Release #1.0, Version #1.30
CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/09/273,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTY: USA
VIP: 10036
CMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPATER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,161
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leglie
RECISTRATION NUMBER: 18,872
REFERENCE DOCKET NUMBER: 1101-176
TELEFONE: (212) 790-990
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTER SCIES:
LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%;
ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-273-685-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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GYWLS 10
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US-08-480-434-31

INCOMPTER 1. Application US/08480434

| Sequence 31, Application US/08480434

| Patent No. 5811248

| Patent No. 5811248

| APPLICANT: Charles C. Ditlow, et al.

| TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS, TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

| TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

| TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

| TITLE OF INVENTION: ANTIBODIES THEREOF

| TOTRES POINTERS:

| ADDRESSEE: ADDRESS:

| ADDRESSEE: ADDRESSEE: ADDRESSEE:

| ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE:

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| ADDRESSEE: 
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-UNN-1995
CLASSIFICATION NUMBER: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
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HYPOTHETICAL: N
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.9%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS: unl
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HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-31
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1 GFWMS 5
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Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

GENERAL INFORMATION:

TYPLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy

TILE REPERENCE: 44137-5023, U. of Tennessee

CURRENT APPLICATION NUMBER: US/09/315,127

CURRENT PILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C Ditlow, et al.
TITLE OF INVENTION: ATHEROSCIEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30, DB 4; Length 667;
Pred. No. 5.8e+02;
1, Mismatches 0; Indels
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZOPETATE TO THE TOTAL STREET TO THE TOTAL STRE
CURRENT FILING DATE: 1999-05-20 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 667
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                                                                                                                                                                                                                                                                                       ; ORGANISM: Artificial Sequence US-09-315-127-5
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.9%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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LENGTH: 667
TYPE: PRT
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                                                                                                                                                                                                                                                TYPE: PRT
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Pred. No. 2e+05;
1; Mismatches 0; Indels
                                                                                                                                                      7606-053
         FILING DAALS

CLASSIFICATION: 435

ATTOCNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (415) 854-360
TELEPHONE: (415) 854-360
TELERAX: (415) 854-3694
TELEX: 66141 PENNIE
07-JUN-1995
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Sequence 11, Application US/08204656B
Requence 11, Application US/08204656B
Retent No. 553882
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Honda, Koichi
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: 011gosaccharide Using The Enzyme
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,451B

FILING DATE: 26-APR-1993

CLASSIFCATION: 424

ATYCKNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 75,227

REFERENCE/DOCKET NUMBER: 7606-033-999

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 415-854-3694

TELEFAX: 415-854-3694

TELEFAX: 6414 PENINE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

LENGTH: 5 amino acids

TENENCH SCALLING ACIDS

LENGTH: 5 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                      NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
STREET: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknow
; MOLECULE TYPE: DNP
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-31
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1 GFWMS 5
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US-08-053-451B-22
US-08-053-451B-22
US-08-053-451B-22
US-08-053-555584

Detent No. 5955584

APPLICANT: Chalch, Francis W.

APPLICANT: Calenoff, Emanuel

TILLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC

TILLE OF INVENTION: ATHEROSCLEROTIC PLAGUE SPECIFIC

TILLE OF INVENTION: ATHEROSCLEROTIC PLAGUE SPECIFIC

CORPUTER: 1155 Avenue of the Americas

TILLE OF INVENTION OF SPECIFIC PLAGUE SPEC
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                         Score 29; DB 2; Length 5; Pred. No. 2e+05; 0; Indels 1; Mismatches 0; Indels
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Pred. No. 2e+05;
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Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
                         87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.9
Best Local Similarity 80.0
Matches 4; Conservative
                                                   Best Local Similarity 80.0 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: N
HYPOTHETICAL: N
HAPOTHETICAL: N
HAPOTHETICAL: N
HAPOTHETICAL: N
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US-08-053-451B-31
                         Query Match
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Gaps
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                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831

FILING DATE: 06-JUN-1995

CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/204,656

FILING DATE: 02-MR-1994

ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 234-252P

TELEPHONE: (703) 205-8000

TELEPHONE: (703) 205-8000

TELEPARATION FOR SEQ ID NO: 11:
CONTRANT SEQ 1D NO: 11:
                                                                                                                                                                                                           Query Match 87.9%; Score 29; DB 1; Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.9%; Score 29;
                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-470-702-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 amino acids
                     LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
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LENGTH: 14 amino acid
   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                     linear
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FRAGMENT TYPE:
US-08-467-831-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT-TYPE CARBOHYDRATE HYDROLASE,
VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
OLIGOSACCHARIDE USING THE ENZYME
1 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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ZIP: 22042

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMpatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,702

FILING APPLICATION: 435

PRICA APPLICATION NUMBER: US 08/204,656

FILING DATE: 02-MAR-1994

ATTOMENY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MIYAIRI, IKUO
APPLICANT: ISHKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HY
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE EN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.9%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-204-656B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 GYWM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
TELEX: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYWM 4
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US-08-470-702-11
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Length 119;
                                                                                                                                                                                                                                MEDIUM TYPE: RIPOPKMIS

MEDIUM TYPE: PLOSPKMIS

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,451B

FILING DATE: C-APR-1993

CLASSIFICATION: 424

ATTONEY/AGENT INPORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 36,426

TELEPAK: 415-854-369

TELEPAK: 6141 PENNIE

INFORMATION FOR SEQ ID NO: 125: SEQUENCE CHARACTERISTICS: LEMGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.9%; Score 29; DB 2; Le. Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 1; Mismatches 0;
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 22, 2003, 12:55:42 Job time : 5.375 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-053-451B-125
                                                                                                                                         COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 GFWMS 35
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                                                  RESULT 14
US-08-053-451B-114
US-08-053-451B-114

Sequence 114, Application US/08053451B
Settle OF UNIVERTION: ATTHERNOSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ATTHERNOSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Ditlow, Charles C.
TIT'LE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF;
NUMBER: OF SEQUENCES: 176
CORRESPON;DENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX. 66141 FENIX
TELEX. 6614
          Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches
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Best Local Similarity 80.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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US-08-053-451B-125
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Gaps

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4
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 12:48:24 ; Search time 18.6607 Seconds (without alignments) 97.882 Million cell updates/sec Run on:

US-09-674-716B-11 98 1 BIRLKSDNYATHYAESVKG 19 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	heavy	Ig heavy chain V r	heavy	heavy	Ig heavy chain V-I	heavy chain	heavy chain	heavy chain	heavy chain	heavy	heavy chain	heavy chain	heavy chain		heavy chain	heavy chain	heavy	heavy	heavy chain	heavy	heavy chain	heavy chain	heavy chain	heavy	heavy chain	heavy chain	noclonal anti		Ig heavy chain V r
QI	S26460	S38714	824521	AVMS06	AVMSAB	AVMS61	AVMS09	AVMSB7	AVMS82	A25803	AVMS57	HVMSAM	MHMS76	PC1213	177394	809958	326462	PH1091	PH1092	A27630	A41940	132513	S67945 🗡	G29380	PH1093	868211	PC4436	PH1293	842467
1 80	2 S		2 8			·	1. A	e.	1	7	7	H	7	2	2	03											~		
% Query Match Length D	101	115	106	115	113	113	113	113	115	115	113	113	111	139	64	121	100	110	110	119	121	141	125	139	110	220	444	119	137
% Query Match	100.0	100.0	4	4.	92.9	ď	2	92.9	92.9	8.06	87.8	86.7	77.0	74.5	69.4	69.4	68.4	68.4	68.4	68.4	68.4	68.4	67.3	66.3	'n	64.3	4.	62.2	62.2
Score	96	86	93	93	91	16	91	91	16	68	86	82	75.5	73	68	9	67	67	67	67	67	63	99	65	64	63	63	61	61
Result No.	-	~	e	4	Ŋ	9	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain V r Ig heavy chain V-I Ig heavy chain V-D Ig heavy chain pre Ig heavy chain pre Ig heavy chain V r Ig heavy chain pre	chain chain chain chain chain chain	
S46466 PL0122 S44107 PH1289 H129380 A31485 B34903	24403 A34903 A34903 SSR213 FH1288 S26926 S00981	ALIGNMENTS
00000000	000000000	
55 100 126 132 118 137	137 137 127 127 100 119	
0.0000000000000000000000000000000000000	58.2 58.2 57.1 57.1 56.1	
55 88 88 8 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1	, , , , , , , , , , , , , , , , , , ,	
0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩	

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Gibeavy chain V region - mouse
Gispecies: Mus musculus (house mouse)
Gispecies: Mus musculus (house mouse)
Gispecies: Mus musculus (house mouse)
Giscession: 826460
BiKavaler, J.
submitted to the EMBL Data Library, April 1991
Ai,Accession: 826460
Ai,Status: preliminary
Ai,Accession: 826460
Ai,Status: preliminary
Ai,Molecule type: mRNA
Ai,Molecule type: mRNA
Ai,Molecule type: mRNA
Ai,Molecule type: mRNA
Cisperfaminy: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
```

ö Gaps ö 100.0%; Score 98; DB 2; Length 101; 100.0%; Pred. No. 1.1e-08; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 19; Conservative

32 EIRLKSDNYATHYAESVKG 50 1 EIRLKSDNYATHYAESVKG 19 임 ઠે

RESULT 2

Systa,

Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S38714
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Reference number: S38714
A;Scatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIMA;Gross-references: EMBL:X76014; NID:g416092; PIDN:CAA53601.1; PID:g1334076
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>

Gaps ö Length 115; Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels

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1 EIRLKSDNYATHYAESVKG 19 49 EIRLKSDNYATHYAESVKG 67 ઠે d

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The state of the s
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Date: 30-Jun-1993 #sequence variation
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; WUID:78158406; PMID:417344
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A; Residues: 1-113 < VRA>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology < IMM>
F;22-98/Disulfide bonds: #status predicted
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C.Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: A90400; A02072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                 Length 113;
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                                                                     92.9%; Score 91; DB 1; I
llarity 94.7%; Pred. No. 1.7e-07;
Conservative 0; Mismatches 1;
F;22-98/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
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                                                                                                         Local Similarity
les 18; Conserv
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Matches 18; Conserv
                                                                         Query Match
                                                                                                                     Best Loca
Matches
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C;Species: Mus musculus (house mouse)
C;Dacte: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 31-Mar-1997
C;Accession: A93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Matl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
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A; Residues: 1-115 <JOH>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
P;15-100/Domain: immunoglobulin homology <IMM>
P;22-98/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Mesidues: 1-113 < VRA>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily a; immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
P; 15-100/ Domain: immunoglobulin homology < IMM>
                                                            S24521

Ig heavy chain V region - mouse

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S24521

R;Kaatrinen, M.

B;Reference number: S24490

A;Reference number: S24490

A;Accession: S24521

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <KAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V-III region (J606) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: C92811, A0211, A0211, L: Hood, L.
R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-bi
A;Reference number: A92811; MUID:82099361; PMID:6798111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X66664; NID:g51247; PIDN:CAA47226.1; PID:g51248 C;Superfamily: immunoglobulin Vegion; immunoglobulin homology C;Keywords: heteroretramer; immunoglobulin F;21-106/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.2e-08;
1; Mismatches 0; Indels
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Local Similarity 94.7%; Pred. No. 7.5e-08;
GB 18; Conservative 1; Mismatches 0; Indels
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Matches 18,
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                                    RESULT 3
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Ig heavy chain V region (AMPC1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18 - Aug-1982 #sequence_revision 18 - Aug-1982 #text_change 31 - Mar-1997
C;Accession: A02073
R;Rudikoff, S; Potter, M.
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n: A;Reference number: A92810; MUID:81216632; PMID:6787122
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 31-Mar-1997
C;Accession: A02074
R;Bernard, O.; Gough, N.M.
R;Bernard, O.; Gough, N.M.
R;Bernard, O.; Gough, N.M.
R;Hitle: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans A;Reference number: A02074; MUID:81013937; PMID:6251474
                                                                                                                                       Ig heavy chain V-III region (T957) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: A92810; A02072
S;Rudikoff, S; Potter, M.
J Immunol. 127, 191-194, 1981
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n
A;Reference number: A92810; MUID:81216632; PMID:6787122
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A; Residues: 1-113 < RUD>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology < IMM>
F; 22-98/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         A Accession: A92810
A Molecule type: protein
A) Rolecule type: protein
A) Residues: 1-13 < RUD>
C) Comment: This chain was isolated from a myeloma protein that binds inulin.
C) Superfamily: immunoglobulin V region; immunoglobulin homology
C) Superfamily: immunoglobulin homology < IMM>
F;15-100/Domain: immunoglobulin homology < IMM>
F;22-98/Disulfide bonds: #status predicted
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A;Residues: 1-111 <BER>
A;Note: the sequence was also determined from the differentiated gene
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89.5%; Pred. No. 1.6e-06;
Mismatches 2; Indels
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89.5%; Pred. No. 1.1e-06;
iive 0; Mismatches 2;
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50 QIRLASDNYATHYAESVKG 68
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Matches 17; Conservative
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hes 17; Conserv
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C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C;Accession: A25803
B;Herbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.
Biol. Chem. Hoppe-Seyler 367, 843-851, 1986
A;Title: The complete amino-acid sequence of the variable domain of a monoclonal anti-st
A;Reference number: A25803; MUID:87076047; PMID:3539142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D92811; A02072

C;Accession: D92811; A02072

J: Tamwunol. 128, 302-307, 1992

J: Tamwunol. 128, 302-307, 1992

A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein A;Reference number: A92811; MUID:82099361; PMID:6798111

A;Reference number: A92811; MUID:82099361; PMID:6798111

A;Residues: 1-115 <-JOH>
A;Residues: 1-115 <-JOH>
C;Comment: This châin was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
F;15-100/Domain: immunoglobulin homology < IMM>
F;22-98/Disulfide bonds: #status predicted
R;Vrana, M.; Rudikoff, S.; Potter, M.
Biochemistry 16, 1170-1175, 1977
A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein. A;Feference number: A90400; MUID:77134726; PMID:402936
A;Accession: A90400
A;Molecule type: protein
A;Residues: 1-113 <VRA>
C;Comment: This chain was isolated from a myeloma protein that binds inulin. C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>F;15-100/Domain: immunoglobulin homology <IMM>F;15-100/Domain: immunoglobulin predicted
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;Species: Mus muscullus (house mouse)
jatte: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
;Accession: D92811; A02072
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A;Residues: 1-115 <HBR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
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94.7%; Pred. No. 1.7e-07;
tive 0; Mismatches 1; Indels
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Matches 18; Conservative
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RESULT 9

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RESULT 10

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Ig heavy chain precursor V region (mAb H8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PC1213
R;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, Gene 121, 331-335, 1992
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc A;Reference number: PC1213; MUID:93077049; PMID:1446832
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: 177394
R;Owens, J.D.
Mol. Cell. Biol. 11, 5660-5670, 1991
A;Title: Non-homologous recombination/deletion at sites within the mouse JH-Cdelta locus A;Reference number: 157520; MUID:92017847; PMID:1922069
A;Note; the sequence of the first 197 residues of the C region was also determined and C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;10-94/Domain: immunoglobulin homology < IMM> F;17-92/Disulfide bonds: #status predicted
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A, Residues: 1-139 < HON-
A, Residues: 1-139 < HON-
A, Crose-references: GB: M98041; NID: G195092; FIDN: AAA38159.1; PID: G195093
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Reywords: heterotecrearer; immunoglobulin
E, 1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region #status predicted <WAT>
F;34-119/Domain: immunoglobulin homology <IMM>
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A,Residues: 1-64 <RES>
A;Cross-references: GB:M64568; NID:g198472; PIDN:AAA39341.1; PID:g198473
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                     Query Match 77.0%; Score 75.5; DB 1; Length 111; Best Local Similarity 89.5%; Pred. No. 5.3e-05; Matches 17; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.00017;
4; Mismatches 1
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Q59029 methanococc
P40355 saccharomyc
P40355 homo sapien
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J. IMMINIO. 128:302-307 (1982).

J. IMMINIO. 128:302-307 (1982).

BINDS INULIN.

PIR, C92811; AVNS06.

HSSP; P01789; IMCP.

InterPro; IPR003596; Ig_WC.

InterPro; IPR003596; Ig_V.

Ffam; PR0047; ig; 1.

SWART; SM00406; IGy.

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22 98 BY SIMILARITY.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-III region A4.
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Local Similarity 94.7%; Pred. No. 1.4e-08;
Les 18; Conservative 1; Mismatches 0;
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MEDIINE-82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L., Hood L.;
The complete V domain amino acid sequences of binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV32 MOUSE STANDARD; FRT; 115 AA. P01801; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) 119 heavy chain V-III region J606.
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SYEZ HELPJ
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HV3F HUMAN
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SEQUENCE.
MEDLINE-78158406; PubMed=417344;
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                                                                                                                                                                                                                  April 22, 2003, 12:46:53 ; Search time 9.5 Seconds (without alignments) 82.953 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112892 seqs, 41476328 residues
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Database :

Result 8

Sequence:

Run on:

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Gaps

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EQUENCE.

YEAR MEDIINES—1815446; PubMed=417344;

WEDDIINES—1815466; PubMed=417344;

Yeana M., Rudikoff S., Potter M.;

"Sequence variation among heavy chains from inulin-binding myeloma proteins.";

"Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

"I Proc. Natl. Acad. Sci. U.S.A. 75:1957-1867(1978).

"I Proc. Natl. Acad. Sci. U.S.A. 75:1957-1867(1978).

"I Proc. Natl. Acad. Sci. U.S.A. 75:1957-1867(1978).

"E PROC. Natl. Acad. Sci. U.S.A. 75:1957-1867(1978).

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Biochemietry 16:1170-1175(1977).
-! MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
BINDS INULIN.
PIR; A90400; AVMSB7.
HISSP; PO1810; 2.FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_WC.
InterPro; IPR003506; Ig_V.
SMART; SMO047; ig; 1.
SMART; SMO0406; IGV.
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22 998 BY SIMILARITY.
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Vrana M., Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                        15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region B109.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 13%, Last annocation update)
15-JUL-1999 (Rel. 38, Last annocation update)
19 heavy chain V-III region ABE-47N.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA; 12647 MW; EESOF2F20EDB129B CRC64;
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P01799;
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MEDLINE=78158406; PubMed=417344;
A Vrana M., Rudikoff S., Potter M.;
A Vrana M., Rudikoff S., Potter M.;
A Vrana M., Rudikoff S., Potter M.;
I Vocella.";
I Sequence variation among heavy chains from inulin-binding myeloma proteins.";
I Proc. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).
I PROC. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).
I MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
I BINDS INULIN.
I RISP, PO18410; ZFBJ.
I I RISP, PO18010; ZFBJ.
I I RICE-Pro; IPR003596; Ig_V.
I RICE-Pro; IPR003596; Ig_V.
I RMART; SM0406; IGV.
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101737;
21-0TU-1986 (Rel. 01, Created)
21-0TU-1986 (Rel. 01, Last sequence update)
15-0TU-1999 (Rel. 38, Last annocation update)
16 heavy chain V-III region U61.
17 heavy chain V-III region U61.

18 heavy chain W-III region Release to the maculus (Mouse).

19 heavy chain W-III region Solutopata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musina
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HV29 MOUSE STANDARD; PRT; 113 AA.
AC P01798; DT 21-UUL-1986 (Rel. 01, Last sequence update)
DT 21-UUL-1986 (Rel. 01, Last sequence update)
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Best Local Similarity 94.77,
Best Local Similarity 18. Conservative
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Best Local Similarity 94.74
Matches 18; Conservative
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P01804;
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P01803;
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HV35 MOUSE
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"Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
evidence for a new heavy chain joining segment.";
- in Immunol. 127:191-194(1981).
- i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 128:302-307(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-82099361; PubMed-6798111;
Obnbson N., Slankard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulin-binding proteins.";
                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels
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01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG heavy chain V-III region T957.
                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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PIR, A92810; AVMS57.

HSSP; P01810; 2FBd.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

Immunoglobulin V region.

DISULFID 22 98 B
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HSSP, P01810, 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SMO0466; IGv; 1.
Immunoglobulin V region.
DISULFID
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          68
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          50 EIRLKSHNYATHYAESVKG
                                                                                                                                STANDARD;
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P01800;
                                                                                                                           HV33 MOUSE
P01802;
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SQUENCE FROM N.A.
MEDINE-81013937; PubMed=6251474;
MEDINE-81013937; PubMed=6251474;
Bernard O., Gough N.M.;
"Nucleotide sequence of immunoglobulin heavy chain joining segments nucleotide sequence of am unonstant regions genes.";
Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
-i. MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-III region HPC76 (Fragment).
18 hus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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  Length 113;
                                            2; Indels
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113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;
Query Match
Best Local Similarity 89.5%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115-JULY Chain V region AMPC1.
Mus musculus (Mouse)
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Best Local Similarity 89.5
Matches 17; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913 (1980).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT PRINDS PROSPHORYLCHOLINE.
PIR; A02070; AVMST5.
HSSP; P01789; 1MCP.
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MEDLINE-80199926; PubMed=6769593;
Early P., Huang H., Davis M., Calame K., Hood L.;
"An immunoglobulin heavy chain variable region gene is generated from three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
                                                                                                                                                                                                Robinson E.A., Appella E.; "Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 11 TaxID=10090;
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
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MEDLINE-81197602; PubMed=7231520;
Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";
Nature 291:29-34 (1981).
-!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.0%; Score 48; DB 1; Length 122; Best Local Similarity 52.9%; Pred. No. 0.43; Matches 9; Conservative 4; Mismatches 4; Indels
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"Slate differences among immunoglobulin heavy chains from
"phosphorylcholine-binding proteins.";
Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;
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MEDLINE=76110488; PubMed=813561;
Rudikoff S., Barstad P., Potter M., Hood L.;
Unpublished results, cited by:
Hood L., Campbell J.H., Blgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
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                                                                                                                                  SEQUENCE.
MEDLINE=81054880; PubMed=6776528;
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MEDLINE=76222762; PubMed=819932;
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SMO0406; IGv; 1.
Immunoglobulin V region.
NON_TER 122
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52 RNKANDYTTEYSASVKG 68
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AC P0178 M
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REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.

BIR; A02074; MHMS76.

InterPro; PR003006; Ig_MHC.

InterPro; IPR00306; Ig_V.

Pfem; PF00174; ig; 1.

SMART; SM00406; IGV; 1.

Immuncoglobulin V region.

NON_TER 1 1 11

SEQÜENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1996 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region IR2 precursor.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
NOBI_TAXID=10116;
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SEQUENCE FROM N.A.
MEDLINE=83064537; PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
Hellman L., Pettersson Of the heavy chain from rat immunoglobulin
"Structure and evolution of the heavy chain from or immunoglobulin
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-!- MISCELIANBOUS: THE MENA WAS ISOLATED FROM AN IGE-SECRETING
IMMUNOCYTOWA THAT ARISES SPONTANBOUSLY IN LOU/C/WSL RAIS.
PIR; A02075; EVRTIS.
                                                                                                                                                                                                                                                                                                                                                                                                               77.0%; Score 75.5; DB 1; Length 111; 89.5%; Pred. No. 1.1e-05; tive 0; Mismatches 1; Indels 1
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003066; Ig_V.
Pfam; PP00047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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69 EIRNKANNYVAYYGKSLKG 87
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ses 17; Conservative
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ID HV01_RAT
AC P01805;
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HV21 MOUSE
ID HV21 MO
DT 21-JUL.
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DT 21-JUL.
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Matches
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   DOTAL BEAR BY A DESTRUCTION OF THE STATE OF 
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HV25 MOUSE
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HV25 MOUSE
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15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16 heavy chain V region HPCM6.
19 heavy chain V region HPCM6.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
15-JUL-1999 (Rel. 03, Last annotation update)
15 heavy chain V region H8.

Mus musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MuschI_TaxID=10090;
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49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels
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MEDLINE-81197602; PubMed=7231520;
Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE
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                           PIR, A02070; AVMST5.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_V.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Hybridoma.
NON_TER 123 123
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P01788;
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P01791;
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ANDLINE-81197602; PubMed=7231520;

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ANDLINE-81197602; PubMed=7231520;

ANDLINE-81197602; PubMed=7231520;

ANDLINE 291.29-34[1981].

ANDLINE 291.29-34[1981].

ANDLINE 291.29-34[1981].

ANDLINE PHOSPHORYLCHOLINE.

BINDS PHOSPHORY 12 MHC.

BINDS PHOSPHORY 12 MHC.

BINDS PHOSPHORY 12 MHC.

BINDS PHOSPHORYLCHOLINE.

R HART; SMOUG40; 1G-W1.

FT NON TER 123 AJ: 13807 WW; AJ584FB098B7785D CRC64;
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RT "IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";

RI Hature 291.29-34(1981).
C -- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.

OR PIR; A02070; AVMST5.
CPIR; A02070; AVMST5.
NR INSP; PO1789; MPC.
DR InterPro; IPR003306; Ig_W.
DR InterPro; IPR003306; Ig_W.
DR SMART; SMO0406; IG_V.
SMART; SMO0406; IGV; 1.
SMART; SMO0406; IGV; 1.
ST NOW TER 123 123
SEQÜENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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49.0%; Score 48; DB 1;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01794;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 heavy chain V region HPCG14.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA.
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Job time : 10.5 secs
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Q93nc6 myxococcus P82987 homo sapien

Q9pz19 xestia c-ni Q96BE5 fritzobium 1 Q96BE5 fritzobium 1 Q34751 bacillus su Q34783 oryza sativ Q97289 plasmodium C69247 bacillus 1i C66071 bacillus 1i C66071 bacillus 1i Q906009 drosophila Q9vj80 drosophila Q9vj80 drosophila Q9vj80 drosophila Q9vj80 drosophila Q9vj80 drosophila Q9vj80 drosophila Q9vj87 atatus norv Q9vj87 atatus norv Q9vj87 drosophila Q9vj87 drosophila Q9vj87 drosophila Q9vj87 drosophila Q9vj87 drosophila Q9vj10 mrosophila Q9vj10 mrosophila Q9vj10 mrosophila Q9vj10 mrosophila

Q921p5 mus musculu Q9pi96 campylobact Q8uOr3 pyrococcus Q918C9 spodoptera Q97kv6 clostridium

OM protein

Run on:

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SEQUENCE FROM N.A.
STRAIN=BALB/C;
MEDLINE=22017847; PubMed=1922069;
MEDLINE=22017847; PubMed=1922069;
MEDLINE=22017847; PubMed=1922069;
Monthomologous recombination at sites within the mouse JR-Cdelta locus accompanies Cau deletion and switch to immunoglobulin D secretion.";
MNO1. Cell. Biol. 11:5660-570(1991).
EMBL; M64568; AAA39341.1; --
HSSP; P01799; 1MCP.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 0.00061;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 AA.
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                     Q9PZ19
Q98BT5
Q96360
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Q960N9
Q9VJ80
P70535
Q9UL88
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O94206
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Q921P5
Q9P196
Q8UOR3
Q9J8C9
                                                      059078
Q94F83
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Q99UF7
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      093NC6
P82987
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                                                                                                                       2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                  JH-Cdelta locus (Fragment)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.4
Best Local Similarity 72.2
Matches 13; Conservative
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                                                              NCBI_TaxID=10090;
NON TER
SEQUENCE
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Q8R3V9
ID Q8R31
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Q61750
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                                                                                                                                                                                                                                                                                                    Q8u651 agrobacteri
Q45562 clostridium
O35037 archaeoglob
Q8tzk5 pyrococcus
Q99zf6 streptococc
P73337 sprechocyst
Q8yck5 brucella me
Q8yck5 anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q61750 mus musculu
Q87349 mus musculu
Q91xel mus musculu
Q91bz2 pseudomonas
Q91bz3 pseudomonas
Q91ds arabidopsis
Q91171 homo sapien
Q8wr61 lymantria d
                                                     April 22, 2003, 12:47:43; Search time 38 Seconds (without alignments) 103.024 Million cell updates/sec
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        GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                             671580 segs, 206047115 residues
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                                        - protein search, using sw model
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Q9RBZ2
Q9RBZ3
Q9FND5
Q9FND5
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Q8U651
Q45962
O35037
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Q99ZF6
P73837
Q8YCK5
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Q8R3V9
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sp_bacteria:*
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Maximum Match 100%
Listing first 45 sv
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Match 1
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01-WAR-201 (TrEMBLrel. 16, Last sequence update)
01-WAR-201 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similarity to heat shock protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
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MEDLINE-98069011; PubMed=9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SEQUENCE FROM N.A.

STRAIN=204180;
MEDLINE=20015131; PubMed=10545263;
Alarcon-Chaidez F.U., Penaloza-Vazquez A., Ullrich M., Bender C.L.;
Characterization of plasmids encoding the phytotoxin coronatine in Pseudomonas syringee."
Plasmid 42:210-220(1999).
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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58.8%; Pred. No. 14;
tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                      50.0%; Score 49; DB 2; Length 361; 52.6%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                             SEQUENCE 361 AA; 41448 MW; 0416AA0203BE5A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Transposase.
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                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Best Local Similarity 58.8 Matches 10; Conservative
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Best Local Similarity
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Q9RBZ3;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLRel. 20, Last annotation update)
Unknown (Protein for IMAGE:4224494) (Fragment).
Mus muschlus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleogtomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090,
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01-MAY-2000 (TYENBLrel. 13, Last sequence update)
01-MAY-2001 (TYENBLrel. 19, Last sequence update)
1S870-11ke transposase.
Pseudomonas syringae (pv. glycinea).
Plasmid p4180A.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pred. No. 4.2;
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Strausberg R.;
Suransherg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO10798; AAH10798.1; -.
InterPro; IPR00407; ig, 4.
PROSTIE; PS00290; IG_MHC, UNKNOWN_2.
NON TER 1
SEQUENCE 480 AA; 51936 WW; 2089234EEF2B41ED CRC64;
                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC024405. AAH24405.1; -. Hypothetical protein. SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AA.
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Best Local Similarity 55.6%
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas.
NCBI_TaxID=318;
[1].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91XE1
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09RBZ2
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1D 09RBZ2
DT 01-M
DT 01-M
DT 01-D
DE 10-D
DE 10-D
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DE 10-D
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Q91XE1
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymantria dispar (Gypsy moth).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Noctuoidea; Lymantriidae; Lymantria.

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                               Gaps
         "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones.";

DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                         46.9%; Score 46; DB 10; Length 2910; 60.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
WLX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                        Q9UL71;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 45.9%; Score 45; DB 4; Length 121; Local Similarity 50.0%; Pred. No. 8.7; Pred 8; Conservative 4; Mismatches 4; Indels
                                                                                     2910 AA; 325351 MW; A847EC3FE1427DF7 CRC64;
                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; APO35043; AAD56279.1; -.
HSCP: PO1772; 2F84.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
Ffan; PFan; PFO047; ig; 1.
NON TER
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                                                                                                                                                                                                                              121 AA
                                                                                                                               2; Mismatches
                                                    EMBL; AB016702; BAB11602.1; -. EMBL; AB017062; BAB11602.1; JOINED.
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51 ISGDGGSTYYADSVKG 66
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                                                                                                                    Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                   297 LKEDNHQEEYAESVE 311
                                                                                                                                                     4 LKSDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                            Heat shock.
  Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                      SEQUENCE
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QBWR61;
                                                                                                            Query Match
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Q9UL71
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MEDINE-21608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SEQUENCE FROM N.A. Denlinger D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P., "Molecular characterization of the insect immune protein hemolin and the high induction during embryonic diapause in the gypsy moth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2160855; PubMed=11743193; Moods D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.9%; Score 45; DB 5; Length 422; 53.3%; Pred. No. 37;
                                                                                                                                         Lymantija dispar.";
Submitted (NOV-2010) to the EMBL/GenBank/DDBJ databases.
BMBL; AR4558681, AAL49765.1;
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig.
InterPro; IPR003069; Ig.MHC.
Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 3.
SWART; SM00409; IG; 3.
SEQUENCE 422 AA; 47234 MW; ODC52EC4BF142617 CRC64;
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EMBL, AE007935; AAK31044.1; -.
Monocxygenase; Plasmid; Complete proteome.
SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nitrilotriacetate monooxygenase, component A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATU6084 OR AGR PTI 161.
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%; Score 45; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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42 EVRFKADNYSTALLE
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Gaps

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Length 182; 2; Indels

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SEQUENCE FROM N.A.
STRAIN-SERJO / ATCC 700294 / SEROTYPE M1;
MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Majar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 43; DB 17; Length 290; 61.5%; Pred. No. 51; ive 1; Mismatches 4; Indels
                                                                                                                 InterPro, IPR001584; Rve.
Pfam, PR00665; rve; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 182 AA; 20733 MW; 860E5DBDE445CDE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amnotation update)
Hypothetical protein PF1986.
                                                                                                                                                                                                                             43.9%; Score 43; DB 17;
58.3%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 AA.
                                                                                                                                                                                                                                                                           3; Mismatches
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MREA OR SPY1250.
Nature 390;364-370(1997).
EMBL; AE001010; AAB89893.1;
EMBL, AE000956; AAB89112.1;
TIGR, AF2135; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 61.5%;
nes 8; Conservative
                                                                                                                                                                                                          Query Match
Best Local Similarity 58...
7, Conservative
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91 DNFKTHHAKKVK 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus.
NCBI_TaxID=2261;
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Matches
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Q99ZF6
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       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
STRAIN-NCIB 7433."
Brehm J.C., Pennock A., Young M., Oultram J.D., Minton N.P.;
Brehm J.C., Pennock A., Young M., Oultram J.D., Minton N.P.;
Physical characterisation of the replication origin of the cryptic
plasmid 0.00101 isolated from Clostridium butyricum NCIB 7423.";
Plasmid 0.0-0(0).
EMBL; X62684; CAA44562.1;
EMBL; X62684; CAA44562.1;
Plasmid 0.0-0(0).
Prove Rep. 1.
Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Frinicutes, Bacillus/Clostridium group, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Length 362;
Pred. No. 45;
2; Mismatches 4; Indels
         Indels
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                   Created)
Last sequence update)
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       5
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                                                                                                                                                                                                             362 AA
       Mismatches
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                  Clostridium butyricum.
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                                                7 DNYATHYAESVK 18
                                                                          ||| |:|:||
57 DNYGQHFADTVK 68
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035037
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Q45962
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MEDLINE=97061201; PubMed=8905231;
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Fasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Syncohovetis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                                                                                     h 43.9%; Score 43; DB 16; Length 310; Similarity 37.5%; Pred. No. 56; 6; Conservative 7; Mismatches 3; Indels
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Pfam; PF01436; NHL; 3.
Hypothetical protein; Complete proteome.
SEQUENCE 474 AA; 53482 MW; 52B2F006F34BE7ED CRC64;
                                                                                                        310 AA; 36047 MW; 4A9A7C575CF2B47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BMBIJ0523.
                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AB006564; AAKA4105.1; -.
InterPro; IPR002606; FAD_Synth.
Pfan; PF01687; FAD_Synth; 1.
ProDom; PP003662; FAD_Synth; 1.
TIGRPANS; TIGR00083; FibF; 1.
Complete proteome.
SEQUENCE 310 AA; 36047 MW; 4A9A7C575CF2B47D C3
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
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87 EVSVKSDAYAEHFLAKPTG 105
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                                                                                                                                                                                                               103 KVSSDHFITHYIKNLK 118
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                                                                                                                                    Query Match
Best Local Similarity
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1D 09YCK
AC 08YCK
DT 01-MA
DT 01-MA
DT 01-MB
DE GBULE
OC BRICE
OC STRAIL
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RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., RA DelVecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G., Rablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., RT Haselkorn R., Kyrpides N., Overbek R.;
RT "The genome sequence of the facultative intracellular pathogen RT Brucella melitensis.";
RT "The genome sequence Sci. U.S.A. 99:443-448(2002).

RR EMBL; Abc005688; AAL53765.1; -D.

RR InterPro; IPR001637; GlnA_adenyltn.

DR InterPro; IPR001637; GlnA_adenyltn.

DR ProDom; Pr00120; gln-synt; l.

RW Ligase; Complete protecome.

SQ SEQUENCE 476 AA; S3095 MW; 9DE8DCIC56471313 CRC64;

Query Match

Best Local Similarity 47.4%; Pred. No. 92;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps

Qy 1 BIRLKSDNYATHYARSVKG 19

Db 261 BAALKHDMYATFWAKPICG 279

Search completed: April 22, 2003, 12:53:52
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Mouse germline hea
Mouse antibody 38C
BW 835 VH. Synthe
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Lead binding MAD 4
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Mouse anti-CD23 MA
Antibody 33F12 cat
Humanised anti-CD2
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                                                                                                                                                                                           April 22, 2003, 12:45:19 ; Search time 48.1786 Seconds (without alignments) 52.550 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAY32263
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98
1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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2G3 hybridoma VH d MAD Br-3 heavy cha MOUSE Br-3 heavy C Br-3 Heavy C Br-3 single chain P5-3 single chain B10,x55-23 bispect Antibody ABX-CBL h MUXINE PSCA antibo MUXINE PSCA antibo MOUSE heavy chain MAD 4197X heavy chain Heavy chain variab Heavy chain variab	Light hybridoma VH Lead binding MAD 7 Scaffold protein S A3 derivative #15, Murine anti-TNFalp Humanised cA2 heav Heavy chain variab Heavy chain variab Amino acid sequenc Mouse heavy chain Anti-TNF antibody Chimeric antibody, Heavy chain variab Mouse MAD 1C11 H C VH region of Ab to 14G1 heavy chain variab Muti-dansy chain variab Muti-dansyl single 8019 VH antibody. H. pylori 26 kDa p H. pylori 26 kDa p	ALIGNMENTS le; 19 AA. lse anti-CD23 MAb C11. lse anti-CD23 MAb C11. lse anti-CD23 MAb C11. neric antibody; humanised antibody; lugar region; CDR; autoimmune disease; lugar serythematosus; multiple sclerosis; diabetes; uveitis; dermatitis; psoriasis; diabetes; uveitis; crohn's disease; psy; asthma; rhinitis; crohn's disease; psy; asthma; rhinitis; diabetes; py. 434.
AAY90812 AAW06212 AAW85059 AAR09423 AAR072870 AAU72866 AAU72864 AAU72864 AAU72874 AAB35297 AAB35297 AAB35297 AAR3696 AAR70829 AAR70829	AAY90816 AA800158 AAB30033 AAY40694 AA881197 AAW28532 AAW40821 AAY2244 AAG7763 AAG7763 AAG7763 AAG7763 AAR12358 AAR12358 AAR12358 AAR12236 AAR12236 AAR12236 AAR12236	ALIGNMENTS 19 AA. anti-CD23 MAb C11. monoclonal antibody; c antibody; humanise region; CDP; autoimm us erythematogus; mu betes; uveitis; derm ne; glomerulonephriti ne; glomerulonephriti ulcarative colitis; asthma; rhinitis; dia
122 142 142 142 143 143 11 143 113 123 123 123 124 124 125 126 127 127 128 129 129 129 129 129 129 129 129 129 129	114 21 119 21 16 20 16 20 110 22 110 22 1119 22 1119 22 1134 12 1134 12 1134 12 113 12 113 14 112 113 14	standard; Peptide; 15 00 (first entry) in CDR H2 of mouse an RII; IgE receptor; me la antibody; chimeric trarity determining ton; arthritis; lupurion; arthritis; dable; nephrotic syndrome; syndrome; allergy; syndrome; allergy; syndrome; allergy; syndrome; allergy; syndrome; allergy; lius. 999; 99WO-GB01434.
9 9 9 9 9 9 9 9 9 9 9 8 8 8 8 4 4 4 4 4	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2258 st 2258; EB-2000 EB-2000 i FCERI clonal almentc ammator's caria; caria; caria; ammator's inoto's caria; ammator's inoto's caria; ammator's caria; ammator's caria; cov. cov. cov. cov. cov. cov. cov. cov.
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AAY03869 AAW46958 AAW01589

AAB50425 AAR34018

Shearin J;

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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody Cl1. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAV32262 and AAV32263), which comprise sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions (see AAV32459) to render them capable of binding to the CD21 type II molecule expressed on capable of binding to the CD21 type II molecule expressed on CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermaities, psoriasis, uriticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ucerative colitis, Crohn's disease, Sjogren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhintis, ecemm, graft-versus-host disease, COPD, insulitis, bronchitis and B-cell malignancies (particularly type II diabetes), and B-cell malignancies (claimed). They are also useful in the binding and various ligands and entity and second continuations between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                       Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 98; DB 21; Length 137; 100.0%; Pred. No. 1.4e-08; ive 0; Mismatches 0; Indels C
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targeted drug delivery.
                                                                                                                                                                                                                         Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB50426 standard; Protein; 286 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 1; 81pp; English.
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                                                        99WO-GB01434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 EIRLKSDNYATHYAESVKG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
18 19; Conservative
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                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                               WPI; 2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137 AA;
                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ34745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200071556-A1.
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                                                        07-MAY-1999;
                                                                                                              09-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000.
  18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB50426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                              COR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibodies, such as primeric of murine anti-CD23 (FCERII) monoclonal antibodies, such as thiered antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain comprise sufficient of the amino acid sequences of Cl1 light and heavy chain c CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematorpoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, crype II molecule expressed on haematorpoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, clabetes, uveitis, dermaitis, psoriasis, uriticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinaic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly from allergies) chief and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                      Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                         represents complementarity determinating region 2 ne heavy chain of murine anti-CD23 (FCERII) monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; dabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; urilammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 98; DB 21; Length 19; 100.0%; Pred. No. 1.4e-09; ive 0; Mismatches 0; Indels
  Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse anti-CD23 MAb C11 heavy chain variable region.
  Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32260 standard; Protein; 137 AA
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78..96
/note= "CDR H2"
129..131
/note= "CDR H3"
                                                                                                                                                                                                                         Claim 1, Page 40; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining the binding agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 19; Conservative
  Bonnefoy JMP, Crowe SJ,
                                                           WPI; 2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AA;
                                                                                      N-PSDB; AAZ34743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY32260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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RESULT 2 AAY32260

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Gaps

"CDR 3"

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                                                                                                                                                                            The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cytocoxic agents, where the antitumour agent is a microtubule stabilising agent such as pacilitaxel, epothilone or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The ketone derivatives are useful for transfeted drug delivery. The inactive molecules in the ketone compounds are converted to active molecules by retro-Michael reaction. The antibody has bifunctional activity and specifically immunoraects with cell surface antigen of a target cell. The active ingredients can be mixed effectively with excipients as per deelired amount along with the buffering agent to enhance the effectiveness and activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 0; Gaps
                                                                                              New ketone compounds containing active agents useful as carriers for e.g. antitumor agents, antibiotics or fluorescent molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urticaria; nephrotic syndrome; glomerulonephritis;
inflammatory bowel disease; ulcerative collitis; Crohn's disease;
Sjogren's syndrome; allergy, asthma; rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 98; DB 22; Length 286; 100.0%; Pred. No. 3.4e-08; ive 0; Mismatches 0; Indels C
            Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69..100
/note= "framework region 3"
101..103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..30 // note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36..49
/note= "framework region
            List B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised anti-CD23 MAb Cl1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32263 standard; Protein; 444 AA.
                                                                                                                                                   Disclosure; Fig 10; 45pp; English.
            Rader C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31..35
/note= "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50..68
/note= "CDR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 EIRLKSDNYATHYAESVKG 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000 (first entry)
                Barbas CF, Shabat D,
                                             WPI; 2001-061339/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AA;
                                                                 N-PSDB; AAC90472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 compound
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This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody Cl1, composed of a human cramework (HSIGRII) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody Cl1. The DNA was constructed by splice overlap FCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimcto's thyroiditis, multiple sclerosis, capadome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Slogren's syndrome, allergic asthma, acute asthmatic exacerbation, rhinitis, ecemen, and Ecell malignancies (Claimed). They are also useful disease, and B-cell malignancies (Claimed). They are also useful determining the binding and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
                                                                                                                                                                                                                                                                                                                                                                                    receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                            Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse germline heavy chain variable (VH) region, V(H)22.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 98; DB 21; 100.0%; Pred. No. 5.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                               /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                           diabetes, multiple sclerosis and psoriasis
                                                                      /note= "constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE06973 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining the binding agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Fig 4; 81pp; English.
                                                                                                                                                                                   99WO-GB01434.
                                                                                                                                                                                                                      98GB-0009839.
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Matches 19; Conservative
                                                  ..444
               ..111
                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                   WPI; 2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 AA;
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ34748.
                                                                                                           W09958679-A1.
                                                                                                                                                                                                                        09-MAY-1998;
                                                                                                                                                                                     07-MAY-1999;
                                                                                                                                                18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                   Region
                                                      Region
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglabulin of human origin. The manised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating thy infection. The proteins of the invention are useful for inhibiting or treating cleaved; autoimmune disorders such as the inhibiting settle of the invention are useful for inhibiting and multiple settle original such as the inhibiting a restences; attenced as the inhibiting restences; attenced as the inhibiting restences; attenced as the inhibiting restences; attenced as a cute inflammatory disorder also useful for treating allergy, anaphylaxis, and for inhibiting estences; actte inflammation, histamine and igg.

The inhibiting and acute inflammatory glomerulopathies, acquired theory, chronic and acute inflammatory glomerulopathies, acquired inmune deficiency syndrome (AIDS), restences as associated with vascular Humanised antibodies are also useful for inhibiting narrowing of the intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, and inhibiting neointimal hyperplasia of the rest of the inhibiting neointimal hyperplasia of the control of 
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multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrocic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatcory glomerulopathy; vascular intervention; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Keefe T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.9%; Score 95; DB 22; Length 100; 94.7%; Pred. No. 3.1e-08; ive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones ST, O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 152-153; 183pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newman W,
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                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                        02-FEB-2001; 2001WO-US03537.
                                                                                                                                                                                                                                                                                                                                                        03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 QIRLKSDNYATHYAESVKG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region, V(H) 22.1
                                                                                                                                                                                                       WO200157226-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larosa GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                         Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB50425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cytotoxic agents, where the antitumour agent is a microrubule stabilising agent such as pacificate, epothilone or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The inactive molecules in the ketone compounds are converted to active molecules by retro-Actobal reaction. The antibody has bifunctional activity and specifically immunoreacts with cell surface antigen of a target cell. The active inspecifients can be mixed effectively with excipients as per desired amount along with the buffering agent to enhance the effectiveness and activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                     New ketone compounds containing active agents useful as carriers for e.g. antitumor agents, antibiotics or fluorescent molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
              antibody 38C2; ketone compound; antitumour; cytotoxic; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody, MAb; hybridoma; lung; adenocarcinoma; mammary; ovary; prostate; polymorphic epithelial mucin; PEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.9%; Score 95; DB 22; Length 29: 94.7%; Pred. No. 1.1e-07; Pred. Roinstches 0; Indels
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                                                                                                                                                                                                                    Lerner
                                                                                                                                                                                                                   m'
                                                                                                                                                                                                                   List
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR34018 standard; Protein; 115 AA.
                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 9; 45pp; English
                                                                                                                                                                                                                   Rader C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 EIRLRSDNYATHYAESVKG 223
                                                                                                                                      24-MAY-2000; 2000WO-US14366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91DE-4133791.
                                                                                                                                                                99US-0318661.
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                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                   Shabat D,
                                                                                                                                                                                                                                             WPI; 2001-061339/07.
N-PSDB; AAC90471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 AA;
                                                                                WO200071556-A1
                                                                                                                                                                25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE4133791-A
                                                                                                           30-NOV-2000
                                                                                                                                                                                                                   Barbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BW 835 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR34018;
                Mouse, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                        Mus sp.
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Gaps

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Length 116;

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binding fragment of the SM3 antibody bound to a peptide recognised by the epitope binding site of SM3. The products and methods can be used to develop agains for the detection of tumour calls and for therapy against tumours. MUCl epitope minics can also be used to prevent or decrease immune response, e.g. in the therapy of diseases caused by autoimmune responses (such as arthritis, multiple solerosis, asthma or disabetes), allergies, inflammatory disorders or transplant rejections such as graft versus host disease. The present sequence represents the amino acid sequence of a heavy chain variable region of SM3 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a branched mucin type synthetic glycolipid. A gene fragment encoding the V region of the heavy chain of an antibody recognising the present protein is claimed. The antibody gene fragment is useful for the development of cancer treatments and diagnosing agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a synthetic branched mucin type glycolipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recognising branched mucin type synthetic glycolipid - using gene fragment of an antibody, useful in cancer treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branched mucin type glycolipid; V region; heavy chain; antibody; cancer treatment; diagnosis.
                                                                                                                                                                                             Score 93; DB 20; Length lire
Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Pages 4-5; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                     AAW46958 standard; Protein; 119 AA.
                                                                                                                                                                                                               94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96JP-0241725,
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                                                                                                                                                                                                                                                                                 1 EIRLKSDNYATHYAESVKG 19
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Matches 18; Conservative
                                                                                                                                                                                                             Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                  50 EIRLKSNNYATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-264850/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
                                                                                                                                                                                116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV22331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP10084963-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW46958;
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                      AAW46958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy; immune response; arthritis; multiple sclerosis; asthma; diabetes; inflammatory disorder; transplant rejection; graft versus host disease.
                                                                                                                                                                                                                                                                    835.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM3 antibody crystal structures - used to develop agents for ating e.g. tumors, autoimmune disorders, allergies, inflammatory
                                                                                                                                                                                                                                                                 Monoclonal antibody BW 835 is produced by hybridoma cell line BW f
The antibody strongly reacts with lung adenocarcinomas and human
mammary-, ovary- and prostate carcinomas. It additionally reacts
with polymorphic epithelial mucin (PEM) but does not react with
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sternberg MJE;
                                                                                                                                                                New monoclonal antibody BW835 specific for tumour antigens useful for diagnosis and treatment of tumours affecting the breasts, ovaries, prostate and lungs
                                                                                                                                                                                                                                                                                                                                                                                                     94.9%; Score 93; DB 14; Length 115; 94.7%; Pred. No. 7.9e-08; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snary D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 279-280; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                Seemann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bates PA, Dokurno P, Freemont PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY03869 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating e.g. tumors, autoimmune disorders or transplant rejection
                                                                                                                                                                                                                                      Disclosure; Fig la; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM3 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIRLKSDNYATHYAESVKG 19
                91DE-4133791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 EIRLKSNNYATHYAESVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                Bosslet K, Pfleiderer P,
                                              (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-204650/17.
                                                                                                                WPI; 1993-127068/16.
N-PSDB; AAQ40046.
                                                                                                                                                                                                                                                                                                                                          normal human tissue
                                                                                                                                                                                                                                                                                                                                                                        115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX31971.
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                11-OCT-1991;
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94.9%; Score 93; DB 19; Length 119; 94.7%; Pred. No. 8.2e-08; ive 1; Mismatches 0; Indels
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91US-0659401.
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                                                                                                                                                                                                                               WPI; 2000-338508/29.
                                                                                                                                                                                   (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                             122 AA;
                                                                                                                                                                                                                                         N-PSDB; AAA38896
                                                                                                                                                                                                                                                                                  treating cancer
                                                                                                                   21-MAR-1986;
08-MAY-1988;
08-FEB-1984;
11-JAN-1985;
11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1991;
                                  Homo sapiens
                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5576184-A.
                                                      US6054561-A.
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                                                                           25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06212;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                          Ring DB;
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                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the heavy chain variable region for monoclonal antibody (Nab) 488, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or meutralising the heavy metals in biological and inanimate systems. It can be used in such compositions as perfumes, commetics, plarameceuticals, health care products, skin treatment products, pesticides, health care products, skin treatment products, pesticides, health care products and production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
                                                                                     Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide;
                                                                                                                                                                                                                                                                                                                          DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.9%; Score 93; DB 18; Length 120; Best Local Similarity 94.7%; Pred. No. 8.3e-08; Matches 18; Conservative 1; Mismatches 0; Indels
                                                              Lead binding MAb 4E8 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2G3 hybridoma VH domain SEQ ID NO:2. ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY90812 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 81; 125pp; English.
AAW01589 standard; Protein; 120
                                                                                                                                                                                                                                                                         Wylie DE;
                                                                                                                                                                                                                  95US-0541373.
95US-0462798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                             96WO-US09258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                         22-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 EIRLKSNNYATHYAESVKG
                                                                                                                                                                                                                                                   (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                        Lopez O, Murray PJ,
                                                                                                                                                                                                                                                                                             WPI; 1997-043140/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAT58263.
                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                  10-OCT-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000
                                                                                                                               Mus musculus
                                                                                                                                                   WO9639518-A1
                                                                                                           heavy metal.
                                                                                                                                                                        12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                      AAW01589;
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AAY90812
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The present invention describes a monoclonal antibody (MAD) (1) that binds to a human breast cancer antigen that is also bound by MAD 454C11 and 52C9 (produced hybridoma ATCC (HB8484 and HB8696, respectively). Also described is a hybridoma that produces (1). (1) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence represents a VH domain derived from a 2G3 hybridoma, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
specific binding assay, affinity purification, drug targeting, toxin targeting, imaging, genetic, therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.9%; Score 93; DB 21; Best Local Similarity 94.7%; Pred. No. 8.4e-08; Matches 18; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAb Br-3 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06212 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           86US-0842476.
88US-0190778.
84US-0577976.
85US-0690750.
94US-0288981.
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                                                                                                                                                                                                                                                                                                                                          95US-0483749.
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Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour
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88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
89US-0382768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89WO-US03852.
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06-JUN-1995; 95US-0466034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 EIRLKSNNYATHYAESVKG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.77
Matches 18; Conservative
                                                                          Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-115825/15.
                                                                                                              WPI; 1999-044574/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA;
                                    (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ08605
                                                                                                                                  N-PSDB; AAV71155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR09423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR09423
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                                                                                                                                                                                                                                                                                                                                                                                The heavy chain variable region (AAW06212) of mouse monoclonal antibody Br-3 is the product of a cDNA clone (AAP149437) isolated from a Br-3 hybridoma cDNA library. MAD Br-3 (IGG1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06211) of B38-1 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chineric antibodies (see also AAW06209-10 and AAW06213-18) can be produced that have specificity to human tumour antigens and can be used for the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                        Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain variable region; murine antibody Br-3; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 18; Length 142;
Pred. No. 1e-07;
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                                                                                                                                                                                            Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                              Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse Br-3 heavy chain variable region.
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                                                                                                                                                                                              Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW85059 Btandard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 15; 102pp; English
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88US-0240624.
88US-0241744.
88US-0253002.
89US-0357641.
89US-0367641.
88US-0240624.
88US-0241744.
88US-0243739.
88US-0253002.
89US-0387641.
99US-0364001.
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0466034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis of human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 EIRLKSNNYATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment; human cancer
                                                                                                                                                                                              Better MD, Chang CP,
                                                                                                                                                                                                                                  WPI; 1997-011249/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 AA;
                                                                                                                                                        (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                      N-PSDB; AAT43437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1989;
21-JUL-1989;
27-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-1988;
13-SEP-1988;
04-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1989;
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                                                                              19-JUN-1989
                                                          04-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Gaps
                                                                                                                                                                                                                                                                                                                                       The present sequence represents the heavy chain variable region of murine antibody Br-3. The sequence was used to create chimeric mouse-human immunogalobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody inG-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytotoxicity to target cells or chimeric antibodies can be used for therapeutic purposes in the
                                                                                                                                                                         Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 20; Length 142;
Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
   Lei S,
                                                                                                                                                                                                                     immunoassay, imaging or antitumour agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Br-3 Heavy Chain V Region (mouse).
   Horwitz AH,
                                                                                                                                                                                                                                                                                   Example 3; Fig 15; 92pp; English.
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Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahopatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; retais; thyroid; bladder; brain; melanona; myelona; Fv; sarcona; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; llB2D10; 6H7E7; 8G7C10; ESSA7; 11B2D10; 6H7E7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; B3B0xP4-13; P4-14; P5-3 tetramerisation domain; 3B10xP5-27; 3B10xP5-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a multifunctional polypeptide comprising a domain with a blinding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
Mayer M, Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                           AAU72870 standard; Protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-2000; 2000EP-0106467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2002 (first entry)
                                                                                                                                                                                                                                      Local Similarity 94.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P5-23 single chain Fv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-055119/07.
N-PSDB; AAS97144.
                                                                                                                                                                                             Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KUFE/) KUFER P.
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72870;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                       Matches
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polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protoxos or helmhiths. The autoimmune diseases, bacteria, fungi, sclerosis, Grave's disease, antkylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72810-AAU72815 represent the NKG2D receptor and the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 EIRLKSNNYATHYAESVKG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
         888888888888
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                                                                                                             The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAD) Br-3. The chimeric antibodies can be used for any purpose for which the original murine MADs can be used, with the advancage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%; Score 93; DB 11; Length 143; 94.7%; Pred. No. 1e-07; ttive 1; Mismatches 0; Indels
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                                                                        Claim 13; Page 123 + Fig 15; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIRLKSDNYATHYAESVKG 19
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Search completed: April 22, 2003, 12:51:16
Job time : 49.1786 secs
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Gaps

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94.9%; Score 93; DB 23; Length 255; 94.7%; Pred. No. 2e-07; ive 1; Mismatches 0; Indels

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SEQ ID NO 4
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Sequence 36, Appli
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Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
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                                                                                             April 22, 2003, 12:53:59; Search time 20.0179 Seconds (without alignments) 76.055 Million cell updates/sec
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Sequence 15,
Sequence 5, A
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Sequence 5,
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Sequence 5,
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Sequence 2
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: \( \text{cgn2} \frac{6} \text{prodata} / 1 \text{pubpaa} / 1808 \text{ NEW PUB. pep:*} \)

2: \( \text{cgn2} \frac{6} \text{prodata} / 1 \text{pubpaa} / 1808 \text{ NEW PUB. pep:*} \)

3: \( \text{cgn2} \frac{6} \text{prodata} / 1 \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

4: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

5: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1807 \text{ PUBCOMB. pep:*} \)

6: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1807 \text{ PUBCOMB. pep:*} \)

7: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1809 \text{ NEW PUB. pep:*} \)

8: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1809 \text{ NEW PUB. pep:*} \)

10: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1809 \text{ NEW PUB. pep:*} \)

11: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1801 \text{ NEW PUB. pep:*} \)

12: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1801 \text{ PUB. COMB. pep:*} \)

13: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

13: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

14: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

14: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)

14: \( \text{cgn2} \frac{6} \text{prodata} / 1 / \text{pubpaa} / 1806 \text{ NEW PUB. pep:*} \)
             GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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1 US-09-840-459-36

1 US-09-840-459-36

1 US-09-564-329A-15

2 US-09-55-113-15

2 US-09-934-771-15

2 US-09-934-771-15

3 US-09-934-77-15

4 US-09-934-77-15

5 US-09-756-301A-5

6 US-09-756-301A-5

6 US-09-756-161A-5

7 US-10-043-450-5

2 US-10-044-554-5

2 US-10-044-534-5

10 US-09-839-666-4

10 US-09-839-666-21
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 301932 segs, 80129803 residues
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                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                               US-09-674-716B-11
98
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Match Length
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27
100
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                                                                                                                                                                     Perfect score:
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y Sequence 4, Application US/09883758

y Sequence 4, Application US/09883758

parent No. US20020058800431

GENERAL INFORMATION:

APPLICANT: Barbat, Doron

APPLICANT: Barbat, Loron

APPLICANT: Barbat, Loron

APPLICANT: Reader, Christoph

APPLICANT: List, Barjamin

APPLICANT: List, Poorenty Allegary

APPLICANT: List, Barjamin

APPLICANT: List, B
```

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GRERAL INCORMATION:

GRERAL INCORMATION:

APPLICANT: Reiter, Owen N.

APPLICANT: Witter, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OP INVENTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REPERENCE: 30435.40514

CURRENT FILING DATE: 2000-05-13

CURRENT FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR PLICATION NUMBER: 09/414,279

PRIOR FILING DATE: 1999-01-12

PRIOR PLICATION NUMBER: 60/071,141

PRIOR PLICATION NUMBER: 60/113,230

PRIOR PLICATION NUMBER: 60/113,230

PRIOR PLING DATE: 1999-02-13

PRIOR PLING DATE: 1999-02-17
                                                                 APPLICANT: MITCH.
APPLICANT: MITCH.
APPLICANT: MITCH.
APPLICANT: GAIffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.4014
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 2000-05-03
FRIOR PELLING DATE: 1999-07-20
FRIOR PELLING DATE: 1999-07-20
FRIOR PILING DATE: 1999-07-30
FRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-02-33
PRIOR FILING DATE: 1998-02-37
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR PELLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR PELICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1999-02-17
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89.5%; Pred. No. 3.8e-07;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-855-153-15; Application US/09855153; Patent No. US20020102666A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIRLKSDNYATHYAESVKG 19
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Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15
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Batent No. US20020058804A1

GENERAL INFORMATION:

APPLICANT: Barbas III, Carlos F.

APPLICANT: Babat, Doron

APPLICANT: List, Benjamin

APPLICANT: Lorner, Richard A.

ITITLE OF INVENTION NUMBER: US/09/883,758

CURRENT APPLICATION NUMBER: US/09/318,661*

FRIOR PILING DATE: 1999-05-25

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 298

TYPE: PRI

CORGANISM: Mus musculus

US-09-883-758-2
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Pred. No. 1.9e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.9%; Score 95; DB 10; Length 100; Best Local Similarity 94.7%; Pred. No. 5.7e-08; Matches 18; Conservative 1; Mismatches 0; Indels
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: WHERE: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
PRIOR PELING DATE: 2001-02-02
PRIOR PAPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR PLING DATE: 1999-07-23
PRIOR PLING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARRE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36
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US-09-564-329A-15
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US-09-883-758-2
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GENERAL INCRMATION.

J. APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435,54US14

CURRENT APPLICATION NUMBER: US/09/963,620

CURRENT FILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-05-03

PRIOR PILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-11

PRIOR FILING DATE: 1999-07-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILICATION NUMBER: 60/124,675

PRIOR FILING DATE: 1998-02-17

PRIOR PILING DATE: 1998-02-17

PRIOR PILING DATE: 1998-03-16

PRIOR PILING DATE: 1998-03-16
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                                                   FRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILLING DATE: 1997-03-10
PRIOR FILLING DATE: 1997-03-10
PRIOR FILLING DATE: 1998-01-12
PRIOR FILLING DATE: 1998-01-12
PRIOR FILLING DATE: 1998-02-13
PRIOR PILLING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/13,230
PRIOR PELLING DATE: 1998-12-21
PRIOR PILLING DATE: 1999-12-17
PRIOR PILLING DATE: 1999-03-16
PRIOR PILLING DATE: 1999-03-16
PRIOR PILLING DATE: 1999-03-16
PRIOR PILLING DATE: 1999-03-16
PRIOR PILLING DATE: 1999-03-10
PRIOR PILLING DATE: 1998-03-10
PRIOR FILLING DATE: 1999-03-17
PRIOR PILLING DATE: 1998-03-17
PRIOR PILLING DATE: 1999-03-17
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; Sequence 15, Application US/09963620
; Patent No. US20020141941A1
; GRERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REPERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/934,773
PRIOR APPLICATION NUMBER: 02001-08-21
PRIOR APPLICATION NUMBER: 2001-08-21
PRIOR FILLING DATE: 2000-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reiter, Robert B.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REPRENCE: 30455.54018
CURRENT APPLICATION NUMBER: US/09/654,811
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VICE. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.9%; Score 91; DB 10;
89.5%; Pred. No. 3.8e-07;
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PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-10
PRIOR PILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR PILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 15
LENGTH: 151
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Patent No. US20020136689A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09854811
Patent No. US20020119157A1
GENERAL INFORMATION:
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Best Local Similarity 89.5
Matches 17; Conservative
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Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type: PRT CORGANISM: SCID Mice US-09-854-811-15
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-934-773-15
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US-09-854-811-15
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LENGTH: 151
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                                                                                                                                                                                                                                                   US-U9-'56-301A-5

Sequence 5, Application US/09756301A

Patent No. US2010027249A1

GENERAL INFORMATION:

APPLICANT: L6, Junming

APPLICANT: L6, Junming

APPLICANT: Claddona, Peter

APPLICANT: Tolddona, Peter

APPLICANT: Siegel, John

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION: Human Tumor Necrosis

TITLE OF INVENTION: Human Tumor Necrosis

TITLE OF INVENTION: Human Tumor Necrosis

FRIOR FILING DATE: 1996-02.10

PRIOR FILING DATE: 1996-12.11

PRIOR FILING DATE: 1994-02-04

PRIOR FILING DATE: 1993-01-29

PRIOR FILING DATE: 1993-01-29

PRIOR FILING DATE: 1993-01-29

PRIOR FILING DATE: 1993-01-29

PRIOR FILING DATE: 1992-03-18

PRIOR FILING DATE: 1991-03-18

PRIOR FILING DATE: 1992-03-18

PRIOR FILING DATE: 1991-03-18

PRIOR FILING DATE: 1992-03-18

PRIOR FILING DATE: 1991-03-18

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Sequence 5, Application US/09927703
GENERAL INFORMATION:
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Knight, David M.
APPLICANT: Knight, David M.
APPLICANT: Knight, David M.
APPLICANT: Siegel, Soctor
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
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        1 EIRLKSDNYATHYAESVKG 19
                                                                       50 EIRSKSINSATHYAESVKG 68
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US-09-756-301A-5
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US-09-927-703-5
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Sequence 5, Application US/10043432

Publication No. US20030054004A1

SERNEAL INFORMATION:

APPLICANT: Lin FORMATION:

APPLICANT: Daddon, John

APPLICANT: Might, David M.

APPLICANT: MIGHT: 1005-01-01

PRIOR APPLICATION NUMBER: U.S. 09/756,398

PRIOR PILING DATE: 1994-10-18

PRIOR PILING DATE: 1994-10-18

PRIOR PILING DATE: 1994-02-04

PRIOR APPLICATION NUMBER: U.S. 08/192,093

PRIOR PILING DATE: 1994-02-04

PRIOR PILING DATE: 1994-02-04

PRIOR PILING DATE: 1994-02-04

PRIOR PILING DATE: 1993-02-04

PRIOR PILING DATE: 1993-03-04

PRIOR PILING DATE: 1991-03-18

PRIOR PILING DATE: 199
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Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 151
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; ORGANISM: Mus Balb/c
US-10-043-432-5
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; ORGANISM: SCID Mice
US-09-963-620-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Utick, Jan
APPLICANT: Daddona, Peter
APPLICANT: Gladdona, Peter
APPLICANT: Aleght, David M.
APPLICANT: Stegel, John
APPLICANT: Stegel, Scott
TILE OF INVENTION: Human Tumor Necrosis Pactor
TILE OF INVENTION: Human Tumor Necrosis Pactor
TILE OF INVENTION: Human Tumor Necrosis Pactor
TILE REPERENCE: 0975-1005-007
CURRENT APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1996-08-12
PRIOR FILING DATE: 1996-08-12
PRIOR FILING DATE: 1996-08-12
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1993-03-03-18
PRIOR FILING DATE: 1993-03-03-03
PRIOR FILING DATE: 1993-03-03-0
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Pred. No. 0.00014;
0; Mismatches 3;
                                     PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 119
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Patent No. US20020132307A1
GENERAL INFORMATION:
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Mus Balb/c
US-09-766-535A-5
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ORGANISM: Mus Balb/c
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US-09-756-161A-5
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APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Ghrayeb, John
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILER REFERENCE: 0975 1005-010
CURRENT APPLICATION NUMBER: US/09/766,535A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-0-18
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR APPLICATION NUMBER: U.S. 08/192,861
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
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                         CURRENT APPLICATION NUMBER: US/09/927,703
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-01-01
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-05
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
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FILING DATE: 1994-02-04
APPLICATION NUMBER: U.S. 08/010,406
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FILE REFERENCE: 0975.1005-013
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Mus Balb/c
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US-09-766-535A-5
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Pred. No. 0.00014;
0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-02-02
PRIOR PLING DATE: 1992-09-11
PRIOR PILING DATE: 1992-03-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 5
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Job time : 20.0179 secs
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Best Local Similarity 84.2%; Pr
Matches 16; Conservative 0;
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; ORGANISM: Mus Balb/c
US-10-043-450-5
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Sequence 5, Application US/10043450

Patent No. US20020141996A1

GENERAL INPORMATION:

APPLICANT: Le, Junming

APPLICANT: Daddona, Peter

APPLICANT: Daddona, Peter

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION NUMBER: U.S. 09/756,398

PRIOR APPLICATION NUMBER: U.S. 09/756,398

PRIOR FILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-10-18

PRIOR PILING DATE: 1994-10-18

PRIOR PILING DATE: 1994-10-18

PRIOR APPLICATION NUMBER: U.S. 08/192,861

PRIOR FILING DATE: 1994-02-04

PRIOR PILING DATE: 1994-02-04

PRIOR PILING DATE: 1994-02-04
                                                                                                                                                                                                                                                               Sequence 5. Application US/10010229

Patent No. US20020114805A1

GENERAL INFORMATION:

APPLICANT: Le, Junming

APPLICANT: Vilcek, Jan

APPLICANT: Daddona, Peter

APPLICANT: Siegel, John

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE REFERENCE: 0975.1005-013

CURRENT APPLICATION NUMBER: US/10/10/229

CURRENT FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 19

SEGTAARE: FastSEQ for Windows Version 4.0
  Best Local Similarity 84.2%; Pred. No. 0.00014; Matches 16; Conservative 0; Mismatches 3; Indels
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US-10-010-229-5
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LENGTH: 119
TYPE: PRT
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US-10-010-229-5
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US-10-043-450-5
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 13:07:14 ; Search time 15 Seconds (without alignments) 102.543 Million cell updates/sec Run on:

US-09-674-716B-3 81 1 RSSKSLLYKDGKTYLN 16

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

2770

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		>	photosystem I prot		14 H	inhibin beta-B cha	glyceraldehyde-3-p	very late antigen-	alpha-glucosidase		lin, vaso	T-cell receptor be	bable IMP d		topoisomerase I -	chemoattractant pr	oprotein lip	끍		Co	roponin -	fibrinogen alpha c	Ig heavy chain DJ	Ig H chain V-D-J r	dihydropyrimidine	mannose-specific l	protein P8 - curle	S-layer protein -		NAD(+)-glycohydrol
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	ä	;	7	~	~	~	~	7	~	7	7	0	N	~	7	7	~	~	~	N	N	7	7	7	7	7	N	~	0	~	0
	Query Match Length		15	16	12	13	10	13	14	15	15	16	11	14	14	15	15	15	10	13	13	15	15	15	15	15	16	16	10	11	12
%	Query		33.3		32.1	30.9	27.2	27.2	27.2	27.2	27.2		25.9	25.9	25.9	2	25.9	25.9	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.1			23.5
	9400) !	27	27	26	25	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20	20	20	20	20	20	20	19.5	19	19	19
	Result No		-	8	ю	4	Ŋ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

T-cell receptor be	hypothetical profe	orf 61.1 - phage T	thymic humoral fac	serum amyloid P-co	inhibin beta-A cha	48K bile/gallbladd	acidic proline-ric	translation elonga	microbial collagen	T-cell antigen rec	alpha-conotoxin MI	214K exoantigen (v	nitrogenase cofact	protein 0F200022 -	T-cell receptor de
PH0930	G83988	G45681	A28719	B20569	S10926	G58501	B29806	PD0441	B26093	847390	NTKNIM	E33098	832677	PA0058	G35141
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12	13	16	80	σ	10	10	11	11	13	13	14	14	15	15	15
23.5	23.5	23.5	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2
19	19	19	18				18	18	18	18	18	18	18	18	18
30	31	32	33	34	35	96	37	38	36	40	41	42	43	44	45

Query Match
33.3%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels

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Gaps

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9 KDGKTYLN 16 4 KDGNXYIS 11 g ઠે

RESULT 2 S09732

photosystem I protein psaJ - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 12-Reb-1993 #sequence_revision 12-Reb-1993 #text_change 16-Reb-1997
C;Date: 12-Reb-1993 #sequence_revision 12-Reb-1993 #text_change 16-Reb-1997
C;Date: 12-Reb-1993 #sequence_revision 12-Reb-1993 #text_change 16-Reb-1997
R;Restence, Na, 1 Hirano, A.; Hiyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990
A;Title: Polypeptide composition of higher plant photosystem I complex. Identification c.
A;Reference number: 809732
A;Molecule type: protein
A;Residues: 1-16 <IKE>
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: C;Genetics:
A;Genetics: C;Genetics: C;Geneti

C; Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

ô Gaps . 0 Query Match
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels

9 KDGKTYLN 16 g ð

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alpha-glucosidase (EC 3.2.1.20) I - Bacillus "thermoamyloliquefaciens" (fragment)
C;Species: Bacillus "thermoamyloliquefaciens"
C;Species: 22.Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998
C;Accession: S21240
R;Suzuki, Y; Yonezawa, K.; Hattori, M.; Takii, Y.
Eur. J. Biochem. 205, 249-256, 1992
A;Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an nice and in structural parameters calculated from the amino acid composition.
A;Reference number: S21202; NUID:92209510; PMID:1555585
                                                                                                                                                                  Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - bovine (fragm C;Species: Bos primigenius taurus (cattle)
C;Species: 27-oct-1995 #sequence_revision 30-Jan-1998 #text_change 03-Jun-2002
C;Accession: S54344
R;Okezaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
B;Okezaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
A;Tetle: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gliant A;Reference number: S54343; MUID:95194333; PMID:7887910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Very late antigen-1 alpha chain - human (fragment)

N.Alternate names: VLA-1 alpha chain
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Species: Aloun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C,Accession: A28018
R,Takada Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3343, 1987
A,Title: The very late antigen family of heterodimers is part of a superfamily of molecu A,Reference number: A94151; MUID:87204112; PMID:3033641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.2%; Score 22; DB 2; Length 13; 50.0%; Pred. No. 2.2e+03; tive 3; Mismatches 0; Indels
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A;Wolecule type: procein
A;Wosidues: 1-15 <SU2>
A;Residues: 1-10 <SU2>
A;Experimental source: strain KP1071
C;Superfamily: alpha-glucosidase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-14 <TAK>
C;Keywords: duplication; heterodimer; membrane protein
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A, Molecule type: protein
A, Residues: 1-13 <OKA>
C, Keywords: oxidoreductase
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Best Local Similarity
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Best Local Similarity
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Matches 3; Conserv
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2 LEXDGRINL 10
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7 LWRDGR 12
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                                                                                                         proceasome chain 1 - rat (fragment)
NyAlternate names: multicatalytic proteinase chain 1
NyAlternate names: multicatalytic proteinase chain 1
Cybecies: Rattus norvegicus (Norway rat)
C;becies: Rattus norvegicus (Norway rat)
C;becies: Rattus norvegicus (Norway rat)
C;becies: Rattus norvegicus (Norway rat)
C;bute: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;butlley, K.S.; Davison, M.D.; Rivett, A.J.
FEBS Lett. 262, 327-329, 1990
A;Titles: N-terminal sequence similarities between components of the multicatalytic prote
A;Reference number: S09082; MUID:90242957; PMID:2335214
A;Reference number: S09082; MUID:90242957; PMID:2335214
A;Restdues: 1-12 < Lilb:
C;Superfamily: multicatalytic endopeptidase complex chain C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     photosystem I protein psaJ - garden pea chloroplast (fragment)
C;Species: chloroplast Pieum sativum (garden pea)
C;Species: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C;Accession: S09733
R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
FEBS Lett. 263, 274-278, 1990
A;Title: Polypeptide composition of higher plant photosystem I complex. Identification (A;Reference number: S09730; MUID:90242987; PMID:2185953
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BA4736
inhibin beta-B chain - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993
C;Accession: B24736
C;Accession: B24736
A;Reference number: A24736; MUD:86042637; PMID:3864157
A;Accession: B24736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.9%; Score 25; DB 2; Length 13; Best Local Similarity 71.4%; Pred. No. 7.1e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 32.1%; Score 26; DB 2; Length 12; Similarity 66.7%; Pred. No. 4.4e+02; 4; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 55.6'
Matche 5; Conservative
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A; Residues: 1-13 <IKE>
C; Genetics:
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Best Local Similarity
Matches 4; Conserv
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2 RDLKTYL 8
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6 WYKDG 11
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Gaps

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ig heavy chain DJ region (clone C68-101) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jo-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1311
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph.
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-14 <MAS>
C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                              [similarity] - Bacillus cereus (strain ts-4) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Bacillus cereus
C; Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C; Dates: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C; Accession: PC2373
R; Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A; Title: Identification of DNA-binding proteins changed after induction of sporulation A; Reference number: PC2369; MUID:95218265; PMID:7766022
A; Accession: PC2373
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C;Species: vaccinia virus
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 31-Oct-1997
C;Accession: A47148 #sequence_revision 12-May-1994 #text_change 31-Oct-1997
C;Accession: A7142 #sequence_revision 12-May-1994 #text_change 31-Oct-1997
C;Bemperer, N; Traktman, P.
J. Biol. Chem. 268, 15887-15899, 1993
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A;Accession: PH0914
A;Molecule type: mRWA
A;Reddues: 1-11 <GOL>
A;Eszidues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node C;Keywords: T-cell receptor
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25.9%; Score 21; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 2; Indels
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Similarity 50.0%; Pred. No. 3.5e+03;
4; Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      probable IMP dehydrogenase (EC 1.1.1.205)
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Quest Local Similarity 36...
Best Local 4; Conservative
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A; Residues: 1-14 < WAS>
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                                                                                                                                                                                                                                                          2 SSKSLLYK 9
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PH1311
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offiner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta phains in Lewis rats with experimental allergial A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          And an accession in the stinal peptide-binding protein, VIP binding protein, pl8 - gu C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C; Accession: A44101
R; Stallwood, D: Brugger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers, J. Biol. Chem. 267, 19617-19621, 1992
A; Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with A; Reference number: A44101; MUID:92406918; PMID:1527080
A; Accession: A44101
A; Residues: Preliminary
A; Rolecule : preliminary
A; Residues: 1-16 &STA-
A; Residues: 1-16 &STA-
A; Residues: Lis &STA-
A; Residues: Lis &STA-
A; Residues: Lis &STA-
A; Rolecule extracted from NCBI backbone (NCBIP:114120)
C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: EF hand; intestine
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Pred. No. 2.7e+03;
0; Mismatches 2; Indels
          5; Indels
          Mismatches
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71.4%;
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Best Local Similarity 71.7.
Local Si Conservative
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Best Local Similarity 36.4%
               4; Conservative
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2 KKTWWKEGVAY 12
                                                             4 KSLLYKDGKTY 14
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               Matches
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Gaps

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A, Title: Biochemical analysis of mutant alleles of the vaccinia virus topoisomerase I ca
A;Reference number: A47146; MUID:93340198; PMID:8393454
A;Accession: A47146
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: I-15 KLEs
A;Cross-references: GB:i13447
C;Superfamily: vaccinia virus DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
A36279
A36279
C;Date: Lumbricus terrestris (common earthworm)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993
C;Jacession: A36279
A;Jitle: Durification and characterization of a chemoattractant from electric shock-indusinakes
A;Reference number: A36279; MUID:90256800; PMID:2160465
A;Accession: A36279
A;Accession: A36279
A;Accession: A36279
A;Accession: C;Ailaniary
A;Residues: 1-15 <JIA>
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                                                                                                                                                                                                                                                   Query Match 25.9%; Score 21f DB 2; Length 15; Best Local Similarity 66.7%; Pred. No. 3.7e+03; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                         Length 15;
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5 KDLRTY 10
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein April 22, 2003, 12:55:49; Search time 24 Seconds (without alignments) 27.651 Million cell updates/sec Run on:

US-09-674-716B-3 81 1 RSSKSLLYKDGKTYLN 16 Title: Perfect score:

Sequence:

Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

822 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARTES	Description	W PEA PINCE	BACTQ P80072	1 RAT P81563 rattus norv	EISFO P46979 eiser	ANAPL P12801	BACTG P49325	P19095 mustelus	P80525	SPI HALRO Q10997 halocynthia	P01521 conus	P54835 canis	ETTM	ANAVA Q44507	P04378	SP34_DICMU P81545 dictyosteli	P56923	P38007	P81095			P20011	P46980	P80526	P81352	P81663	P31720	20_BRANA P81096 brassica na	P80620	QUAC	COXO RAT P80432 rattus norv	RANCA P22689	TOTA NICOL
	E .	PSAJ	MALT	MM01	MY14	FIBA	SLAP																						1 40		8	1 TK	Ę
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RESULT 2
MALT BACTO

ID MALT BACTO

AC P80072;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 24, Last sequence update)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

OS Bacillus thermoamyloliquefaciens

OS Bacillus thermoamyloliquefaciens

OS Bacillus thermoamyloliquefaciens

ON NCBI TaxID=1425;

RN (1)

RP SEQUENCE

RC STRAIN=KP1071 / FERN P8477;

RX MEDLINE=92209510; PubMed=1555585;

RA SUZUKI Y., YONEZAWA K., HATLORI M., Takii Y.;

SEQUENCE.
STRAIN=KP1071 / FERM P8477;
MEDLINE=92209510; PubMed=1555585;
Suzuki Y., Yonezawa K., Hattori M., Takii Y.;

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conus conso pigeon pea oncorhynchu scyliorhinu scyliorhinu gadalus aca camplubact locusta mig microplitis conus famil physcomitre zea mays (m				; Tracheophyta; eudicots; Rosidae;		÷	psaF			0; Gaps
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P56 0 055 0 051 0 051 0 051 0 051 0 051 0 051 0 051			(Fragment)	Pisum sativum (Garden pea). Pisum Chloroplast. Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid	Vicieae; F	н		Transmembrane	CRC64;	Length 13; ; Indels
			e) ate) (PSI-J)	yophyta , core		tosys	of the	Trang		
	ស	AA.	ed) sequence update) annotation update) er subunit IX (PSI	ptophyta; Embryc eudicotyledons;	idea	Y.; pho	o uo		POTENTIAL. 9E2E45D11FDE3B41	DB 1; 1.7e+02 hes
CCA TO THE TO TH	ALIGNMENTS	13	ed) sequence update) annotation updat er subunit IX (F	rta; otyle	lionc	noue plant aK ge	organization	HE PSAJ FAMILY. Photosynthesis;	IAL. DilFi	ore 25; DB ed. No. 1.7 Mismatches
CXA1 CONCN RS19 PPWBB MILT ONCKE OXYA SCYCA OXYA SQUAC SYK CAMUP LMT4 LOCMI MPI MICOC CXA1 CONGE FGR1 CANFA PGGR1 PHYPA UC19 MAIZE	ALIG	PRT;	quence u notation subunit	tophy	Papi	3; i, Ii her] id ps	rgan	PSAJ	POTENTIAL. 9E2E45D11F	
CXA1 RES19 MILT OXYA OXYA SYK LIMT4 MILT CXA1 FGF1 FGF1 UCLA		ц	ed) sequanno	trep	ae;	18595 ama T hig	the c	THE Pho		-
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144 113 113 113 113 113 113 113 113 113		STANDARD;	15, C 15, L 41, L	(Garden pea) idiplantae; Magnoliophy	3; Fa	PubMe A., sitio psaI,	-278(help	LONGS 3. syste	>13 13 1516	vat
19.8 118.8 118.5 1		STA	(Rel. 15, Created (Rel. 15, Last sed (Rel. 41, Last am I reaction center	(Gard ridip	Fabales, Fabaceae, Papilionoideae, 1888;	987; j irano compo n of j	3:274 May]	Y: BELONGS S 809733. Photosystem	13 AA;	30. Similarity 71. 5; Conservative
				vum tt. Vi	= 38 = 38	242 H, H	26 ON:	RIT 33,	13	imil O
16 16 15 15 15 15 15 15		T 1 PEA PSAJ PEA	01-AUG-1990 01-AUG-1990 11-JUN-2002 Photosystem	Ford. Pisum sativum (Garden pea). Chloroplast. Eukaryota; Viridiplantae; Stre Spermatophyta; Magnoliophyta;	eurosids I; Faba NCBI_TaxID=3888; [1]	SEQUENCE. MEDLINE-90242987; PubMed=2185953; Ikeuchi M., Hirano A., Hiyama T., Inoue Y.; Polypeptide composition of higher plant photosystem "dentification of psal, psad and psak gene products."	FEBS Lett. 263:274-278(1990) -!- FUNCTION: May help in th	<pre>subunits!- SIMILASITY: BELONGS TO THE PSAJ FAMILY PIR; S09733; S09733. Chloroplast; Photosystem I; Photosynthesis</pre>	TRANSMEM NON TER SEQÜENCE	
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		RESULT PSAJ_P	888888	38888	888	R R R R R R R R R R R R R R R R R R R	된임	888 888 888	E E S	OME

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Myoactive tetradecapeptide (ETP).
Eisenia foetida (Common brandling worm) (Common dung-worm).
Eukaryota, Metazoa, Annelida, Clitellata, Oligochaeta, Haplotaxida,
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Gut;
MEDLINE=96087879; PubMed=8532604;
WRena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel gut tetradecapeptide isolated from the earthworm, Elsenia foetida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides 16:995-999(1995).
-1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
                                                                                                                                                                                                                                                                                                         Lumbricina; Lumbricidae; Eisenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.7%;
75.0%;
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MOD RES 14
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Matches 3, Conservative
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND SYNTHESIS.
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              4 KSEKNADFKD 13
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ID MY14 EISFO
AC P46979;
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2 FKDG 5
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FIBA_ANAPL
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MEDLINE-96201136; PubMed-8605638;

TISSUE-Heart,

TYAGI S.C. (1cut)dens J.P.M.;

RT "Myocardial collagenase: purification and structural

RT characterization.";

RT "Myocardial collagenase: purification and structural

RT characterization.";

RT Cardiol. 12:165-17(1996).

C. -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN

THE HELICAL DOWAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY

MATRY PROTEINS DURING THE ONSET OF DIALATED CARDIOMYOPATHY.

C. MATRY PROTEINS DURING THE ONSET OF DIALATED CARDIOMYOPATHY.

C. CAPLYTIC ACTIVITY: Cleaves preferentially one bond in native-

C. CAPLY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR

C. CAPLY PROTEINS DURING THE ONSET OF DIALATED CARDIOMYOPATHY.

C. CAPLY A ROLE IN THE DETERIORATION OF THE ADDIAL TO COLLAGENS OF THE MATRY ENGLISH OF THE ADDIAL THE
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                  alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence and in structural parameters calculated from the amino acid
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY'2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
(MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                          Eur. J. Biochem. 205:249-256(1992).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
PIR, $21240; $21240.
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Pred. No. 6.6e+02;
2; Mismatches 5; Indels
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  "Assignment of Bacillus thermoamyloliquefaciens KP1071
                                                                                                                                                                                                                                                                                      15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA.
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36.4%;
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                                                                                                                                                                                                                                                Hydrolase; Glycosidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                               4 KSLLYKDGKTY 14
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Best Local Similarity
Matches 4; Conserv
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                                                                                         composition.";
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P81563;
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NON TER
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-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIRSTNOGEN TO FIRSTN IS TRIGGERED BY THROWEIN, WHICH CLEAVES FIRSTNOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE PORMATION OF THE SOFT CLOT.
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE=85168193; PubMed=3983613;
Min Y., Ping Z., Yaoshi Z.;
"Purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anas platyrhynchos (Domestic duck).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBI_TaxID=8839;
                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
Score 20; DB 1; Length 14;
Pred. No. 1.4e+03;
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                                                                                      1; Mismatches
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PEPTIDE 1 15
MOD_RES 1
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SEQUENCE.
TISSUE=Hemolymph;
MEDLINE=96321313; PubMed=8759295;
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                                                                                                                                                                                                                                                                                                                             S KSLIF 9
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Q10997;
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 16, Last sequence)
Serum amyloid P-component (SAP) (Fragment).
Mustelus canis (Smooth dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          component.";
J. Balol. Chem. 258:3889-3894(1983).

-I. SUBJUATT: HOMOPENTAMER, PENTAXIN (OR PENTRAXIN) HAVE A DISCOID ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.

-I. DISEASE: SAP IS A PRECURSOR OF ANYLOID COMPONENT P WHICH IS POUND IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.

-I. SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robey F.A., Tanaka T., Liu T.-Y.; "Isolation and characterization of two major serum proteins from the dogfish, Mustelus canis, C-reactive protein and amyloid P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90078111; PubMed=2592346; MEDLINE=90078111; PubMed=2592346; Luckevich M.D., Beveridge T.J.; Luckevich M.D., Beveridge T.J.; Characterization of a dynamic 3 layer on Bacillus thuringiensis."; J. Bacteriol. 171:6656-6667(1989).
-!- FUNCTION: THE S-LAYER IS A PARACKYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINOW: THE SURFACE OF BACTERIA.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH OBLIQUE (P2) SYMMETRY.
                                                                                                                            Gaps
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                                                                    Score 20; DB 1; Length 15;
Pred. No. 1.5e+03;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
S-layer protein (Surface layer protein) (Fragment).
Bacillus thuringiensis (subsp. galleriae).
Bacteria; Firmicutes; Bacillales; Bacillaseae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell wall; S-layer.
NON TER 10 10
SEQÜENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;
                       D78A51FF88B40373 CRC64;
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MEDLINE=83160932; PubMed=6403520;
  15 15
15 AA; 1580 MW;
                                                                       h 24.7%;
Similarity 36.4%;
4; Conservative
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Best Local Similarity
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2 GKTF 5
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SEQUENCE
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Biochem. Biophys. Res. Commun. 213:169-174(1995).
-!- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDILINE-95366993; PubMed=7639732;
TKalcivic J., Ashman K., Meeusen E.;
"Fasciola hepatica: rapid identification of newly excysted juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) [Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fasciola hepatica (Liver fluke).
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
NCBI_TaxID=6192;
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22.2%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                         Query Match 22.2%; Score 18; DB 1; Length 9; Best Local Similarity 60.0%; Pred. No. 1.1e+05; Matches 3; Conservative 2; Mismatches 0; Indels
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Stolidobranchia; Pyuridae; Halocynthia.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Serine proteinase inhibitor (Fragment)
Halocynthia roretzi (Sea squirt)
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14 AA.

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STANDARD;
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-1- TISSUE SPECIFICITY: Expressed by the venom duct.
-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
                                                                   Comp. Biochem. Physiol. 1148:1-9(1996).
-- PUNCTION: STRONGY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
-- SUBUNIT: MONOMER.
-- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
INLEPTO: IRROBOOLS: Serpin. PARILY.
PROSTIE: PS00204; SERPIN. PARILAL.
Serpin; Serine proteage inhibitor; Glycoprotein; Plasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEY
Shishikura F., Abe T., Ohtake S.-I., Tanaka K., Is an orteinase "Purification and characterization of a 58,000-Da proteinase inhibitor from the hemolymph of a solitary ascidian, Halocynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 1; Length 14;
Pred. No. 3e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                            10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-conotoxin MI (M1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01784; NTKNIM.
HSSP; P56973; 1B45.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
3 8
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Similarity 75.0%;
3; Conservative
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Best Local Similarity 75.v.
3; Conservative
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9 GKNY 12
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SEQUENCE
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MEDLINE=91099370; PubMed=2269306;

REDPET S., Linder D., Ellermann J., Thauer R.K.;

Rospert S., Linder D., Ellermann J., Thauer R.K.;

Rospert S., Linder D., Ellermann J., Thauer R.K.;

Reductionly distinct methyl-coenzyme M reductases in

Methanobacterium thermoautotrophicum strain Marburg and delta H.";

Bur. J. Bloochem. 194:871-87(1990)

-I- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)

ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate

to methane and an hetezodisulfide.

-I- CATALYITC ACTIVITY: CH(3) -S-COM + H-S-HTP = CH(4) + COM-S-S-HTP.

-I- COFACTOR: THE BNZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)

TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
BE-TUFFE-LA SUBFAMILY.
HSC-2DPAGE; P54835, DOG.
INTERPROFIES, P54835, DOG.
INTERPROFIES, PROU0795; EF GTPbind.
PROSITE; PS00301; EFACTOR GTP; PARTIAL.
ELONGATION factor; Protein biosynthesis; Mitochondrion; GTP-binding.
NON TER.

14 14 14

SEQÜENCE 14 AA; 1600 MW; 8CAF0B6AE7CCDE41 CPFC44.
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SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
                                                                                                                                                                                                                                                                  TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2133).
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                                                                                                                                                                                                                                                                                                                                                                dog heart proteins.";
Electrophoresis 18:2795-2802 (1997)
-!- FUNCTION: THE PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
--- PUNCTION: THEN THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanobacterium thermoautotrophicum (strain Marburg / DSM 2:
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaccae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
Blongation factor Tu, mitochondrial (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 AA.
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2 SVIYLD 7
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                                                                                                                GON1 PETMA
P04378;
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                                                                                                                                                                                                                                                                                                                                                                      brain."
                                                                                      RESULT 14
GON1 PETMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- MISCELLANDROUS: BELONGS TO THE NIF! GENE CLUSTER WHICH IS EXPRESSED IN HETEROCYSTS UNDER ANAEROBIC AND AEROBIC CONDITIONS.
-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
-1- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
Methanogenesis; Oxidoreductase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyanobacterium.";
Proc. Natl. Acad. sci. U.S.A. 92:9358-9362(1995).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE
BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE
INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PCC 7937 / ATCC 29413;
MEDLINE=96016168; PubMed=7568132;
Thiel T., Lyons B.M., Exter J.C., Ernst A.;
"A second nitrogenase in vegetative cells of a heterocyst-forming
                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cysteine desulfurase 1 (RC 4 4 4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifsl) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena
NCBI_TaxID=1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%; Score 18; DB 1; Length 15; ilarity 50.0%; Pred. No. 3.3e+03; Conservative 2; Mismatches 1; Indels
                                                                                                                     Score 18; DB 1; Length 14;
Pred. No. 3e+03;
                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Monnerighn U., Boehme H.;
Submitted (DC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AA; 1684 MW; 08B8F106DE65547D CRC64;
                                                                          14 14 14
14 AA; 1557 MW; 97E9439C4223B871 CRC64;
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PROSITE; PS00595; AA TRANSFER CLASS 5; PARTIAL.
Nitrogen fixation; Lyase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                   15 AA.
                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                  22.2%;
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                                                                                                       Guery Match
Beet Local Similarity 37.55,
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NIS1_ANAVA
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MEDLINE=86160192; PubMed=3514603; Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.; "Primary structure of gonadotropin-releasing hormone from lamprey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Petromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI TaxID=7757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 261:4812-4819(1986).
-!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND POLLICLE-STIMULATING HORMONES.
-!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                      Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17, DB 1; Length 10;
Pred. No. 3.1e+03;
1; Mismatches 2; Indels
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI TaxID=31287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
1E4B36237B1735AB CRC64;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                        20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA.
10 AA.
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PRT;
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InterPro; IPR002012; GnRH.
Plan; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
Hormone; Amidation; Hypothalamus.
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57.1%;
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STANDARD;
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Best Local Similarity
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Schreiner S.J.;
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1D 242_DICMU
DT 15-JUL
DT 15-JUL
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DE SULFAC
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Gaps

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Best Local Similarity Matches 3; Conserv

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FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KDG 11

Db 6 KDG 8
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Search completed: April 22, 2003, 13:13:03 Job time : 25 secs

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Local Similarity 100.
Les 5; Conservative
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117.741 Million cell updates/sec
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                                                                                                                                                               April 22, 2003, 13:10:19 ; Search time 28 Seconds
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_invertebrate:*
5: sp_invertebrate:*
5: sp_invertebrate:*
6: sp_organelle:*
7: sp_organell
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Q9S8R5
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sp_bacteriap:*
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Match Length DB
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17 20 24.7 16 4 Q9UCI8 Q9uci8 homo sapien 18 19 23.5 9 4 Q9UXJ6 G9UXJ6 G9UXJ6 homo sapien 20 21 19 23.5 11 13 Q9UMJ6 G9UXJ6 G9UWJ2 G9UW
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## ALIGNMENTS

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O61331

O6131

D O6131

D O6131

D O6131;

DC O6131;

DC O6131;

DC O6131;

DC O6131;

DC O1.way-1996 (TrEMBLrel. 01, Created)

DC O1.way-1999 (TrEMBLrel. 10, Last sequence update)

DC O1.way-1999 (TrEMBLrel. 20, Last annotation update)

DC O1.way-1999 (TrEMBLrel. 20, Last annotation update)

DC O1.way-1999 (TrEMBLrel. 20, Last annotation update)

DC O1.way-2002 (TrEMBLrel. 20, Last annotation update)

DC O1.way-2002 (TrEMBLrel. 20, Last annotation update)

SC Mus musculus (Mouse).

C Dukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Musn.

RN '12

NCBI_TAXID=10090;

RN '12

RN '13

RN '14

ANARAZAWA K., Ando T., Kimura T., Narimatsu H.;

RN '15

NEDINE-89033997; PubMed=3141392;

RN '11-length ODNA of mouse N-

RT acetylglucosamine (betal-4)galactosyltransferase.";

RT acetylglucosamine (betal-4)galactosyltransferase.";

RT acetylglucosamine (betal-4)galactosyltransferase.";

RT J. Biochem. 104:165-168(1988).

DR EMBL; D00115; BAA00217.1; ...

KW Glycosyltransferase; Transferase.

RT 1 1 1

RT 1 1

CHYTYL 15

Duery Match

SC SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;

Ouery Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

PRESULT 2

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RESULT 2

RESULT 2

DR RESULT 3

DR
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FTRAINEDIOS;
Leimkunbler S., Klipp W.;
Leimkunbler S., Klipp W.;
Leimkunbler S., Klipp W.;
The molybdenum cofactor biosynthesis protein MobA from Rhodobacter capsulatus is required for the activity of molybdenum enzymes binding MCD, but not for xanthine dehydrogenase harbouring the MPT cofactor.";
FEBS Lett. 174:239-246(1999).
EMBL, AJ131528; CAB43542.1;
NON_TER
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                                                                                                                                                                                                                     Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 11; Length 12;
Pred. No. 3.5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 28.4%; Score 23; DB 2; Length 16; Local Similarity 83.3%; Pred. No. 3.2e+03; nes 5; Conservative 0; Mismatches 1; Indels
                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Molybdopterin cofactor biosynthesis protein C C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA; 1692 MW; 1DFB0534394788F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA; 1445 MW; 84E7876609572735 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mutant DNA polymerase beta (Fragment).
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA.
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           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
27.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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STRAIN=ICR; TISSUE=BRAIN;
Shuichi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1061;
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                                                                                                                                                                         (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q91YFS;
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091YF5
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1D 091YI
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DT 01-DI
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Q16141
ID Q161-
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                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    "Protein database for several tissues derived from five instar of slikworm.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-2025451; PubMed-10760572;
White G.R.M., Varley J.M., Heighway J.;
"Genomic structure and expression profile of LPHH1, a 7TM gene variably expressed in breast cancer cell lines.";
Blochim. Biophys. Acta 1491:75-92(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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MEDILINE=99153747; PubMed=10030676;
White G.R.M., Varley J.M., Heighway J.;
"Isolation and characterisation of a human homologue of the latrophilin gene from a region of 1p31.1 implicated in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h
Similarity 57.1%; Pred. No. 6.5e+02;
8; Conservative 1; Mismatchea
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                                                                                                                                                                                                                                                                                                     STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
MEDLINE=21177481; Pubmed=11280994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 15
15 AA; 1877 MW; 580F6BD4703CA70C CRC64;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annocation update)
Unknown protein from 2D-page (Fragment)
Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Latrophilin-2 (Fragment).
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NON_TER 15 15
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1 YEDNKPFI 8
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                                                                                                                         Query Match 27.2%;
Best Local Similarity 55.6%;
Matches 5; Conservative
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Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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5 EEGRUYL 11
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MEDLINE=92209510; PubMed=1555585;
Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
Nassignment of Bacillus Hermoamyloliquefaciens KP1071 alpha-
"Assignment to E Bacillus Hermoamyloliquefaciens and its striking
glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
and in structural parameters calculated from the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                            Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             MEDINE=94220089; PubMed=7545922;
Sadakane Y., Maeda K., Kuroda Y., Hori K.;
"Identification of mutations in DNA polymerase beta mRNAs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Muricoidea, Muricidae, Rapana.
NCBI_TaxID=29165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94007762; PubMed=8403854;
Idakieva K., Severov S., Svendsen I., Genov N., Stoeva S.,
Beltramini M., Tognon G., Di Muro P., Salvato B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.2%; Score 22; DB 2; Length 15; 36.4%; Pred. No. 4.4e+03; ative 2; Mismatches 5; Indels
                                                                                                                                                                                                                         Score 22; DB 4; Length 13;
Pred. No. 3.8e+03;
2; Mismatches 3; Indels
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                                                                                                                                                                                              SEQUENCE 13 AA; 1568 MW; D88C62798C9542CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MXY-2000 (TrEMBLrel. 13, Created) 01-MXY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 15, Last annotation update) Hemcoyanin RHSS1 subunit (Fragment) Rapana thomasiana (Marine snail)
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
EXO-alpha-1,4-glucosidase (EC 3.2.1.20) (Fragment).
                                                                                                                              patients with Werner syndrome.";
Blochem. Blophys. Res. Commun. 200:219-225(1994)
EMBL; S69873; ABD14051.1; -.
NON TER. 1
                                                                                                                                                                                                                                                                                                                                                                                                       15 AA.
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                                                                                                                                                                                                                            27.2%;
37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                            9 KDGKTYLN 16
                                                                                                                                                                                                                                                                                                              3 RDSAVYIN 10
                                 NCBI_TaxID=9606;
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Q9TWR6
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STRAIN=CV. ALWARO; ITSSUE-LEAF;
MEDLINE=20435797; PubMed=10874039;
Yamaguchi K., von Knoblauch K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 37:28455-28465(2000).
--- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 168 RIBOSOMAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=94378189; PubMed=7916494;

Kalb K., Santoso S., Unkelbach K., Kiefel V., Mueller-Eckhardt C.;

Kalb K., Santoso S., Unkelbach K., Kiefel V., Mueller-Eckhardt C.;

Kalb K., Santoso S., Unkelbach K., Kiefel V., Mueller-Eckhardt C.;

Incalization of the Br polymorphism on a 144 bp exon of the GPIa gene and its application in platelet DNA typing.";

Thromb. Haemost. 71:651-654(1994).

EMBL: $72155; ApD14096.1; -.

NON TER 1

SEQÜENCE 16 AA; 1968 MW; B31EFE05E038C26A CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
"Structural properties of Rapana thomasiana grosse hemocyanin: isolation, characterization and N-terminal amino acid sequence different dissociation products.";

Comp. Biochem. Physiol. 106B:53-59(1993).

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SEQUENCE 15 AA; 1735 MW; 78985413C9E90B6B CRC64;
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Pred. No. 4.8e+03;
3; Mismatches 1; Indels
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Pred, No. 4.4e+03;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Chloroplast 30s ribosomal protein S14 beta (Fragment).
Spinacia oleracea (Spinach).
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Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
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OKSTAGO (14579) TYPE STRAIN;
OKSTAGO (14579) FURMEd=10589720;
OKSTAGO (14579) FURMED HILL B., Rose M., Lereclus D., Kolsto A.B.;
"Sequence analysis of three Bacillus cereus loci under PICR-regulated genes encoding degradative enzymes and enterotoxin.";
Microbiology 145:3129-3138(1999).
BMB., AJJA311; CAB69804.1; -.
SEQÜENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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    "Major histocompatibility complex class I presentation of exogenous and endogenous protein-derived peptides by a transfected human monocyte cell line.";
Immunology 86:606-611(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brugia pahangi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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NCBI_TaxID=1396;

    [1]
    SEQUENCE FROM N.A.
    Emes R.D., Thompson F., Devaney E.;
    A novel mRNA up-regulated in mammalian-derived microfilaria

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 2; Length 11;
Pred. No. 6.7e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                                          Score 21, DB 7, Length 15, Pred. No. 6.5e+03; insmatches 3; Indels
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277990; CAB93515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
Phosphatidylinositol-specific phospholipase C (PI-PLC)
                                                                                                                                                                    15 AA; 1838 MW; 98DCDCC01F8F7E15 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Mmc1 protein (Fragment).
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50.0%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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les 4; Conserv
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Q9NFK8
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C -1 - SUBCELLULAR LOCATION: CHICROPLAST.

-1 TISSUB SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

-1 MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PI. S14 ALPHA AND SEAS PECTYCOMETRY:

-1 MASS SPECTYCOMETRY: NW=11745.9; METHOD=ELECTROSPRAY.

-1 MASS SPECTROMETRY: NW=11747; METHOD=ELECTROSPRAY.

-1 MASS SPECTROMETRY: NW=11747; METHOD=MALDI.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS NW IS: 14 KDA.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS NW IS: 14 KDA.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS WA IS: 18 KDA.

R INTERPRO; IPRO01209; Ribosommal_S19.

INTERPRO; IPRO01648; Ribosommal_S19.

R Pfam: PRO0273; Ribosommal_S19.

R ROSITE; PS00067; RIBOSOMAL S18; PARTIAL.

R RIDOSOMAL S18; PARTIAL.

R RIDOSOMAL D10-CEIN; Chloroplast; RNA-binding.
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Submitted (APR-2000) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: LYS-|-XAA, INCLUDING
LYS-|-PRO.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S5 (SERINE PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
101-JUN-2000 (TrEMBLrel. 15, Last annotation update)
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annopation update)
Fraction 60=HLA BC locus class 1-bound peptide (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21, DB 2; Length 15;
Pred. No. 6.5e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 8; Length 12;
Pred. No. 5.1e+03;
3; Mismatches 2; Indels
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MEDLINE-96165039; PubMed=8567028;
Harris P.E., Colovai A.I., Maffei A., Liu Z., Foca N.S.;
                                                                                                                                                                                                                                                                                                                   NON TER 12 12
SEQUENCE 12 AA; 1513 MW; 5E84D3F10116D057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA; 1483 MW; 3F42C5E66C4F76DD CRC64;
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Similarity 75.0%;
3; Conservative
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NON TER 15 15
SEQUENCE 15 AA; 1483 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 44.4 tes 4; Conservative
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UDN-2000 (TrEMBLrel. 14, Last annotation update)
61-UDN-2000 (TrEMBLrel. 14, Last annotation update)
60-887pium hirshtum (Upland cotton).
60-887pium hirshtum (Upland cotton).
61-827pium hirshtum (Upland cotton).
62-827pium hirshtum (Upland cotton).
63-827pium hirshtum (Upland cotton).
63-827pium hirshtuphyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
63-827pium hirshtuphyta; Malvaceae; Gossypium.
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MEDLINE=94004990; PubMed=8401609;
Andrawis A., Solomon M., Delmer D.P.;
"Cotton fiber annexins: a potential role in the regulation of callose
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                                                                                                                                                                                Query Match 24.7%; Score 20; DB 5; Length 14; Best Local Similarity 45.5%; Pred. No. 8.8e+03; Matches 5; Conservative 2; Mismatches 4; Indels
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Plant J. 3:763-772(1993).
SRQUENCE 15 AA; 1689 MW; 1087950BAC4F69F9 CRC64;
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14 AA; .1602 MW; 5C4C62C55AB89397 CRC64;
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April 22, 2003, 12:54:59 ; Search time 73 Seconds (Without alignments) 29.206 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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81
1 RSSKSLLYKDGKTYLN 16
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Light chain CDR L1	Light chain CDR1 o	Human Kappa II lig	Peptide CDR-L1 der	Murine derived ant					
SUMMARIES	TD	AAY32254	AAW39818	AAW39815	AAW39824	AAW39875	AAW39839	AAW39821	AAU70328	AAY14404	AAB86292
	DB	21	19	19	19	19	19	19	23	20	22
	Query Match Length DB	16	16	16	16	16	16	15	16	16	16
di	Query Match	100.0	95.1	95.6	95.6	85.2			75.3		
	Score	81	77	75	75	69	69	62.5	61	9	59
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(GLAX ) GLAXO GROUP LTD.

ĕ	Sequence of an ant	MAP	Human light chain	Mouse mAb 1D9 anti	CDRL1 region of L	Anti-human Fas mon	ı Fas	Humanised anti-Fas	Murine 13H10 light	CDR1 of the light	Mouse antibody var	Mouse antibody 13G	Murine anti-PI-3,4	Mouse Kappa II lig	Sequence from the	VL sequence of ant	CDR-1 of the L cha	Murine CD4/CD34 re	CDR1 of the light	Anti-platelet glyc	Murine antibody 52	6D9 antibody light	Mouse 6D9 catalyti	L27eY catalytic an	Sequence of light	Complementarity de	3HIS catalytic ant	antibody	H-2Kd MHC-Class I	gat	MAb 3B9 light chai	Anti-Fas MAD HFE7A	the Light	Light chain CDR to
	13					19			21 AAY9216	13	16		22 AAB9719	23		16	19	21	13	21	22	15	22	22 AAG6446	14 AAR4021	22		23	22 AAB8217	22	16	19 AAW8302	20	
9 72.8 1	57 70.4 16	5 67.9 1	5 67.9 1	5 67.9 1	3 65.4 1	3 65.4 1	3 65.4 1	3 65.4 1	2 64.2 1	1 63.0 1	9 60.5 1	9 60.5 1	9 60.5 1	59.3	7 58.0 1	6 56.8 1	6 56.8 1	56.8	55.6	55.6	55.6	53.1	53.1	1 50.6	49.4	0 49.4	9 48.1	9 48.1	•	4 42.0	2.5 40.1	40.1	2.5 40.1	2.5 40.1
11	17	13	14	15	-	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42 3			

## ALIGNMENTS

CD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; soriasis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; slograft-versus-host disease; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR L1 of mouse anti-CD23 MAb C11. AAY32254 standard; Peptide; 16 AA. 99WO-GB01434. 98GB-0009839. 15-FEB-2000 (first entry) 07-MAY-1999; 09-MAY-1998; WO9958679-A1 Mus musculus 18-NOV-1999. AAY32254; AAY32254 

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AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic caid from 3H-phenyl occaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoceter transition state analogue. Antibody 6A12 has a per minute KCat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA; benzoic acid, phenyl cocaine; immunogenic conjugate, reduction; cocaine; treatment,
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     far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.1%; Score 77; DB 19; Length 16; 93.8%; Pred. No. 2.4e-06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain CDR1 of catalytic antibody 3B9.
                                                                                Claim 13; Page 81; 147pp; English.
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                            simply binding
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Matches
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                                                                                                                                                                                                                                                                                   cross of the light chain of murine anti-CD23 (FCERII) monoclonal antibodies, such as chimeric or unanised antibodies, which comprise authodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain corps (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD3 formation for treatment of arthritis, cupus expressed on haematopoietic cells. The antibodies are used to block soluble CD3 formation for treatment of arthritis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative collisis, Crohn's disease, Sjogren's syndrome, allergies, allergies, asthma, intrinaic asthma, acute asthmatic exacerbation, rhinitis, eccema, graft-versus-host disease, CODD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly fornoic bronchitis) or diabetes (particularly fornoic bronchitis) or diabetes), and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                 Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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                                                                                                                                                                                                                                                                  This sequence represents complementarity determinating region (CDR L1) of the light chain of murine anti-CD23 (FCERII) monoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 81; DB 21; Length 16; 100.0%; Pred. No. 5e-07; ive 0; Mismatches 0; Indels
  Shearin J;
  Rapson NT,
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Ellis JH,
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                                                                                                                                                                                                              Claim 1; Page 40; 81pp; English.
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  Bonnefoy JMP, Crowe SJ,
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                                                      WPI; 2000-053101/04.
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                                                                             N-PSDB; AAZ34739
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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSAs, and has a per minute Kcat of 0.16. The antibodies particularly for the treatment of an overdose. They are used for treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                  Length 16;
                                                                                                                                                            Score 75; DB 19; Length 16
Pred. No. 5.2e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain CDR1 of catalytic antibody 12H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 83; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                               AAW39824 standard; peptide; 16 AA.
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                                                                                                                                                                Query Match 92.6%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                16 AA;
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simply binding
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AAW39975-77 represent the sequences of the light chain complementarity determining regions (CDRs) of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found to have CDRs of the present sequence. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                Light chain CDR1 of a catalytic antibody capable of degrading cocaine.
                                                                                                                                                                                                                         Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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87.5%; Pred. No. 5.4e-05;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "not specified"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                        AAW39875 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                    (first entry)
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16
                 1 RSSRSLLYRDGKTYLN 16
RSSKSLLYKDGKTYLN
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Score 75; DB 19; Length 16; Pred. No. 5.2e-06; 2; Mismatches 0; Indels

ch 1 Similarity 87.5%; 14; Conservative

Query Match Best Local Similarity Matches 14; Conserv

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02-MAY-2000; 2000US-0563222.
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overdose; addiction.
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                                                                                                                                                                                                                                                                                                                         simply binding
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                                                                                                                        25-JUN-1997;
                                                          WO9749800-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vařiable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 5.4e-05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain CDR1 of catalytic antibody 2A10.
                                                                                                         Light chain CDR1 of catalytic antibody 8G4E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW39821 standard; peptide; 15 AA.
               AAW39839 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK.
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81.2%;
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-077166/07.
                                                                                                                                                                                    overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                           16-JUN-1998
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                                             AAW39839;
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Matches
 AAW39839
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AAW39921-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                              New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 82; 147pp; English.
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                                                                                                                                                                           (UYCO ) UNIV COLUMBIA NEW YORK.
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97WO-US10965.
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Length 16;

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Neutralized antibody partial peptide derived from hepatitis C virus - useful for inhibiting Hepatitis C Virus (HCV) serine protease activity
                                                                              Disclosure; Page 14; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0297451
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                                                                                                                                                                                                                                                                                                                                       17-AUG-1999 (first entry)
     (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                Query Match 75.3
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                             1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                          1 RSSQSLLHSDGDTYLN 16
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                               WPI; 2002-055482/07
                   Hein MB;
                                                                                                                                                                                                                     16 AA;
                                                                  preparing array
                                                                                                                                                                                                       the invention.
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                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                   Hiatt AC,
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rhis invention describes novel antibodies (Ab) in which the variable region (VR) of at least one chain and/or the VR of at least one heavy chain includes at least one of 7 specified sequences, or fragments of these sequences, or contain at least one light chain and/or heavy chain encoded by specific nucleic acid sequences (I) and (II), reproduced, or their fragments. The products of the invention have antitumor and immunomodulatory activity. Ab, or other antibodies that recognize the same antigen, are used: (i) to identify cognate antigens, comparation, e.g. in an extracorporeal system; (iii) for generating additional antibodies able to label PC; and (iv) for treating autoimmune diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or plastocytoma. Ab are specific for mature PC, i.e. they do not recognize plastocytoma. Ab are specific for mature PC, i.e. they do not recognize plastocytoma. Ab are specific for mature procursors are used as immunogens. Cherospeutic agents, they should show fewer side effects than conventional chemotherapeutic agents. This sequence represents the Wue-1 antibody
                                                         This sequence represents a peptide derived for the sequence of the light chain variable region complementarity determining region (CDR)-1 of the anti-hepatitis C Virus (HCV) Ser/Thr procease monoclonal antibody (MAb) 8D4 protein. The invention relates to the use of partial peptides (AAVI4348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; Wue-1; variable region; light chain; heavy chain; antitumor; immunomodulatory; cognate antigen identification; autoimmune disease; tumor; multiple myeloma; lymphoma; plastocytoma; CDR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies specific for plasma cells, useful for treatment and diagnosis of autoimmune diseases and plasma cell tumors
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                                                                                                                                                                                                                                                                                         Score 60; DB 20; Length 16
Pred. No. 0.0018;
1; Mismatches 2; Indels
                     Example 1; Page 13; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB86292 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MUEL/) MUELLER-HERMELINK H K.
                                                                                                                                                                                                                                                                                               74.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99DE-1062583.
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                                                                                                                                                                                                                                                                                                                         Local Similarity 80.0
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                1 RSSKSLLYKDGKTYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSSKSLLHSDGNTYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller-Hermelink HK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-426596/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GREI/) GREINER A.
                                                                                                                                                                                                                                               16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE19962583-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB86292;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                activity.
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                           The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides calls), comprising using a library of two different polynucleotides to encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and at least 75% sequence identity to a framework region (RR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                        Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity determining region; CDR; monoclonal antibody; MAb; hepatitis C virus; HCV; protease; binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 23; Length 16;
Pred. No. 0.0012;
2; Mismatches 2; Indels
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Sequences AAB73652-AAB73654 represent, respectively, CDRs 1-3 of the light chain variable region (LH) of antibody IOR C5.
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                                                        16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP491351-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                               AAR24704;
                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a chimeric antibody, or an Fv-type single-chain fragment, derived from the murine monoclonal antibody or an ingle-chain fragment, derived from the murine monoclonal antibody confidence of the CDRs 
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant antibody, or single-chain fragment, derived from murine monoclonal IOR C5, useful for treatment and diagnosis of colo-rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody IOR C5; hybridoma ECCC 97061101; mouse; humanised; IOR C2 antigen; colorectal cancer; tumour; metastasis; therapy; drug targetting; imaging; diagnosis; eytostatic; VL; light chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mateo De Acosta Del Rio CM, Roque Navarro LT, Morales Morales A;
Perez Rodriguez R, Ayala Avila M, Gavilondo Cowley JV;
Duenas Porto M, Bell Garcia H, Rengifo Calzado E, Iznaga Escobar N;
Ramos Zuzarte M;
                                                                                                                                      Gaps
  variable region light chain complementarity determining region CDR1 fragment described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        Murine monoclonal antibody IOR C5 light chain variable region CDR1
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0
                                                                                             Score 59; DB 22; Length 16; Pred. No. 0.0027; 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                          AAB73652 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 24; 30pp; Spanish.
                                                                                               72.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2000; 2000WO-CU00004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99CU-0000196.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                             Query Match 72.8
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                        1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                              1 KSQSLLDSDGKTYLN 16
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                                                            16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
Synthetic.
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                             AAB73652;
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of an anti-human fibrin antibody light chain variable
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     Length 16
                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric monoclonal antibody, anti-fibrin antibody, antithrombotic agent, myocardial infarction therapy
Score 59; DB 22;
Pred. No. 0.0027;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tada H;
                                                                                                                                                                                                                                                                                                          AAR24704 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taka H, Watanabe T,
  72.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region chain designated 'A'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0121591
                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1992 (first entry)
  Query Match 72.8
Best Local Similarity 75.0
Matches 12; Conservative
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                                                                                                                                                  1 KSSQSLLDSDGKTYLN 16
                                                                                                               1 RSSKSLLYKDGKTYLN 16
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Tsurushita

Paul SM,

Bales KR,

2000US-0184601

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New humanised antibody for the treatment of Alzheimer's comprises the inhibition and reduction of the formation of amyloid plagues
                                                                                                                                                                                                                                          Claim 14; Page 45; 63pp; English.
                                                                                     08-DEC-2000; 2000US-0254465.
                                                       26-FEB-2001; 2001WO-US06191.
                                                                                                                                                     Holtzman DM, Demattos R,
                                                                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                               ELIL ) LILLY & CO ELI
                                                                                                                                                                                    WPI; 2001-550087/61.
             WO200162801-A2
                                                                           24-FEB-2000;
                                30-AUG-2001
                                                                                                                                                                Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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ID AAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity determining region; CDR1; Hu266; nootropic; neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; antibody; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR30448-50 represent the kappa chain and AAR30451-53 the heavy chain complementarity determining regions (CDR of a monoclonal antibody (MAD), C242:II. C242:II is a monoclonal murine Ab of IgG class produced when culturing in an appropriate medium a hybridoma cell line obtained by fusing spleen cells from a mouse, which has been immunised with a human colonic adenocarcinoma cell line, with the murine myeloma cell line Sp2/0. C242:II when bound to a cell surface antigen is capable of being endocytosed or
                                                                                             Kappa; chain; heavy; complementarity determining region; CDR; MAb; monoclonal antibody; C242:II; murine; IgG; hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                            Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing hybridoma cell line C242:11 or mutants, useful for diagnosis and therapy of pancreatic or colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human light chain complementarity determining region, CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 14; Length 16;
Pred. No. 0.013;
2; Mismatches 2; Indels
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            AAR30448 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                  Lind P, Lindholm L;
                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 11; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%;
                                                                          C242:11 MAb kappa chain CDR1
                                                                                                                                                                                                                    92EP-0850166
                                                                                                                                                                                                                                         91SE-0002074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                      (first entry)
                                                                                                                                                                                                                                                            (KABI ) KABI PHARMACIA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 73.3
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internalised into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSSKSLLHSNGNTYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSSKSLLYKDGKTYL 15
                                                                                                                                                                                                                                                                                                       WPI; 1993-002345/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA;
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Synthetic.
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                                                      06-MAY-1993
                                                                                                                                                                                                                                                                                   Holmgren J,
                                                                                                                                endocytosis.
                                                                                                                                                                                              07-JAN-1993
                                                                                                                                                                         EP521842-A.
                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                AAR30448;
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AAR30448
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The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, beta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of coluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is human light chain CDR1 (complementarity determining region 1) used to humanise the mouse monoclonal antibody 266 to produce Hu266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; graft rejection; CC chemokine receptor 2 antagonist; CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant; lung transplant; pancreas transplant; bowel transplant; heart-transplant; graft versus host disease; chronic graft rejection; antibody light chain; mAb 1D9; CDR1; complementarity determining region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse mAb 1D9 antibody light chain complementarity determining region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 22; Length 16;
Pred. No. 0.013;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.98;
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les 10; Conservative
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1 RSSQSLIYSDGNAYLH 16
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YI
Inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft, involves administering a CCR2
Tradegonist -
Tradegonist
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Query Match 67.9%; Score 55; DB 23; Length 16; Best Local Similarity 68.8%; Pred. No. 0.013; Matches 11; Conservative 3; Mismatches 2; Indels Qy | RSSKSLLYKDGKTYLN 16 | | | | | | | | | | | | | | Db 1 KSSQLLDSDGKTFLN 16

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Gaps

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Search completed: April 22, 2003, 13:12:32 Job time : 74 secs

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US-09-835-087-14
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LENGTH: 16
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Sequence 8, Appli
Sequence 2, Appli
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Sequence 4, Appli
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Sequence 16, Appli
Sequence 16, Appli
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Sequence 497, App
Sequence 692, App
Sequence 693, App
Sequence 694, App
Sequence 694, App
Sequence 694, App
Sequence 695, App
Sequence 674, App
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                                                                                                     April 22, 2003, 13:13:30 ; Search time 41 Seconds (without alignments) 31.270 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/DCT NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-518-737-8

US-09-79-744-8

US-10-091-236-14

US-10-091-236-4

US-10-091-226-4

US-10-091-226-4

US-09-879-461-16

US-09-879-461-16

US-09-879-461-16

US-09-879-461-16

US-09-876-94A-343

US-09-809-638-497

US-10-084-813-692

US-10-084-813-694

US-10-084-813-694

US-10-084-813-694

US-10-084-813-694

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                                                                                                                                                                                                                                                                                                  301932 seqs, 80129803 residues
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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20 26 32.1 12 10 US-09-850-351A-61 Sequence 61, Appl 22 2.2 26 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 23 26 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 25 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 26 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 26 32.1 16 9 US-09-736-969-193 Sequence 18, Appl 26 32.0 10 10 US-09-780-053-670 Sequence 344, Appl 27 30.9 10 10 US-09-780-053-670 Sequence 103, Appl 27 30.9 10 10 US-09-780-053-670 Sequence 103, Appl 30 25 30.9 11 9 US-09-969-037-1 Sequence 37, Appl 30 25 30.9 11 9 US-09-969-037-2 Sequence 27, Appl 31 25 30.9 12 9 US-10-161499-26 Sequence 37, Appl 32 25 30.9 15 9 US-10-161499-26 Sequence 27, Appl 32 25 30.9 15 9 US-10-161499-26 Sequence 27, Appl 33 25 30.9 15 9 US-10-161499-26 Sequence 27, Appl 34 24 29.6 15 9 US-10-216-408-25 Sequence 25, Appl 36 24 29.6 15 10 US-09-96-288-13 Sequence 25, Appl 36 24 29.6 15 10 US-09-96-288-13 Sequence 25, Appl 36 24 29.6 16 9 US-09-996-288-13 Sequence 27, Appl 41 23.5 29.0 11 10 US-09-96-13 Sequence 113, Appl 42 23.5 29.0 11 10 US-09-96-13 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 27, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-96-288-105 Sequence 26, Appl 54 29.6 15 0 US-09-96-288-105 Sequence 27, Appl 54 29.6 16 0 US-09-96-288-105 Sequence 26, Appl 54 29.6 16 0 US-09-96-288-105 Sequence 27, Appl 54 29.6 16 0 US-09-96-288-105 Sequen
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## ALIGNMENTS

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US-09-835-087-14

US-09-835-087-14

US-09-835-087-14

US-09-835-087-14

US-0520020042370A1

GENERAL INFORMATION: Method of Treating Graft Rejection Using

TITLE OF INVENTION: Method of Treating Graft Rejection Using

TITLE OF INVENTION: Method of Treating Graft Rejection Using

TITLE REPREMENCE: 1855.2008-003

CURRENT PAPLICATION NUMBER: 105/943,448

FRIDE REPREMENCE: 1855.2009-004-14

CURRENT FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGRAISM: Wise Musculus

SEQ ID NO 14

LENGRAISM: Mus Musculus

SEQ ID NO 14

COGANISM: Mus Musculus

SEQ ID NO 14

SEQ ID NO 14

COGANISM: NORMATION: CDR1 of murine mab ID9 light chain variable region

US-09-835-087-14

QUECY Match

GOGANISM: Mismatches 2; Indels 0; Gaps

OF IRSTRICTORM: 15

Best Local Similarity 68.8%; Pred. No. 0.007;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps

OF IRSTRICTOR OF US200008321A1

SEQUENCE 8, Application US/09518737

SEQUENCE 8, Application US/09518737

APPLICANT: SHIRAL, RAUCHI
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Sequence 14, Application US/10091236

Batent No. US20020168360A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
TITLE OF INVENTION: DISORDERS BY ADMINISTERING INFEGRIN ALPHA-V-BETA-3 ANTAGONISTS
TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS
TITLE OF INVENTION: UNMERS: US/10/091,236
CURRENT APPLICATION WUMBER: US 60/273,098
PRIOR APPLICATION WUMBER: US 60/273,098
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION WUMBER: US 60/316,321
PRIOR APPLICATION WUMBER: US 60/316,321

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 14

SEQ ID NO 14

SEQ ID NO 14

SEQ ID NO 14
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Sequence 4, Application US/10091313

Sequence 4, Application No. 202030044406A1

Sequence 4, Application No. 2020300044406A1

GENERAL INFORMATION:

APPLICANT: DINGIVAN, CHRISTINE

TITLE OF INVENTION: DISORDERS BY ADMINISTERING CD2 ANTAGONISTS IN COMBINATION WITH OF TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

CURRENT APPLICATION NUMBER: US/10/091,313

CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR PELICATION NUMBER: US 60/273,098

PRIOR FILING DATE: 2001-03-02

PRIOR PELICATION NUMBER: US 60/346,918
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Pred. No. 2.1;
6; Mismatches 2; Indels
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                                              CURRENT APPLICATION NUMBER: US/09/796,744
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: UP 2000-59508
PRIOR FILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFWARE: PALENTIN VEY: 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative 6
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Best Local Similarity 61...
8; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-796-744-8
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ORGANISM: Mus sp.
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Sequence 29, Application US/09217268B
Patent No. US20020065398A1
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Frias, Ernesto M
APPLICANT: 1999-12-21
NUMBER OF SEQ ID NOS: 36
APPLICANT: Frias APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: SHOJI, EMI
APPLICANT: SAKUADA, MIKKIKO
APPLICANT: FURUYA, AKIKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NIWA, RINPEI
APPLICANT: SHIBATA, KENJI
APPLICANT: SHIBATA, KENJI
APPLICANT: SHIBATA, KENJI
APPLICANT: YAMASAKI, MOTOO
TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
FILE REPERRNCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR PILING DATE: 1999-09-03
SOFTWARE: PATENT VET. 1999-09-03
SOFTWARE: PATENT VET. 1999-09-03
SOFTWARE: PATENT VET. 1999-09-03
SOFTWARE: PATENT VET. 10
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Pred. No. 0.62;
6; Mismafches 2; Indels
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Pred. No. 0.068;
5; Mismatches 2; Indels
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OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-29
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Patent No. US20020098527A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-8
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ORGANISM: Murine
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US-09-217-268B-29
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LENGTH: 15
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ADDRESSE: SmithKline Beecham Corporation
STRET: Corporate Intellectual Property, UW2220 - 709
SCITY: King of Prussia
                                                                                 ö
                                                                                                                                                                                                                                                                                 APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Mitchell S.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/612,929
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/612,929
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/612,929
FILING DATE: LA-OCT-1993
ATTORNEY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 15
                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32.5; DB 9;
Pred. No. 33;
6; Mismatches 2;
                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                               Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                    US-09-879-461-16;
; Sequence 16, Application US/09879461;
; Publication No. US20020193575A1;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/10205150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.1%;
                                                 48.1%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: (215) ;
(215) 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 43.8
Matches 7; Conservative
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                                               Query Match
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                        1 RSSQSLAKSYGNTYLS 16
; OTHER INFORMATION: LDP-02
US-09-748-960-9
                                                                                                                  1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-879-461-16
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US-10-205-150-4
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LOCATION: (1)...(16)
OTHER INFORMATION: CDR1 of the light chain of antibodies Act-1 and
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Patent No. US20010046496A1

GENERAL INFORMATION:
APPLICANT: Bretten. Lee R.
APPLICANT: Foxt, Judith A.
APPLICANT: Allison, David Edward
TILE OF INVENTION: Method of Administering an Antibody
FILE REFERENCE: 1855.2007-001
CURRENT FILING DATE: 2000-112-27

PRIOR APPLICATION NUMBER: US 09/550,082

PRIOR PILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 9

LENTH: 16
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                                                                                                                                    DB 9; Length 16;
                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3;
2; Mismatches
                                                                                                                                                                      2; Mismatches
                                                                                                                                      Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%;
 NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                    48.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.1
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                    Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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                                                                    ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-091-313-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus sp.
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                                                   LENGTH: 16
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Sequence 928, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CAR.
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; TITLE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SQC ID NOS: 1242
; SOFTWARE: Patentin Version 3.1
; TENGRE PATENTIN VERSION 3.1
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Publication No. US20030068615A1
GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR PLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR PLICATION NUMBER: US 60/151,270
PRIOR PLILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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          APPLICANT: Arthur B. Raitano
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
TILE REFERENCE: 129.35US01
CURRENT APPLICATION NUMBER: US/09/809,638
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 746
SEQ ID NOS: 746
SEQ ID NO 497
                                                                                                                                                                                                                                                                                                                                                                                                     35.8%; Score 29; DB 9;
55.6%; Pred. No. 81;
ative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-809-638-497
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2 YKEGHNYEN 10
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                                                APPLICANT: LINGNAU, KAREN ET AL.

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR IMMUNOMODULATION AND PREPARATION
TITLE OF INVENTION: OF VACCINES COMPRISING AN ANTICEN AND AN IMMUNOGENIC OLIGODECXIN
TITLE OF INVENTION: AND A POLYCATIONIC POLYMER AS ADJUVANTS
FILE REFERENCE: SONN:018US
CURRENT APPLICATION NUMBER: 120/2-05.150
CURRENT FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: PCT/EP01/00087
PRIOR FILING DATE: 2001-01-05
NUMBER OF SCO ID NOS: 9
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-876-904A-343

Sequence 343, Application US/09876904A

Sequence 343, Application US/09876904A

Publication No. US20030072794A1

GENERAL INPORMATION:

APPLICANT: BOULIKAS, TENT

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TW) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSGENIC PEPTIDE

FILE REPRENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR PILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOUTHARE: Patentin Ver. 2.1

SEQ ID NO 343

LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-205-150-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 32; DB 9; Length 9; 62.5%; Pred. No. 2.7e+05; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Ser/Thr protein kinase US-09-876-904A-343
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Publication No. US20030059895A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Saccharomyces cerevisiae
Publication No. US20020197269A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity
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6 YRDHKTHLH 14
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Sequence 693, Application US/10084813
; Sequence 693. Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYEPPTIDES THAT BIND HIV GP120 AND RELATED NUCLBIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REPREENCE: 218975
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT PILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 693
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                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-693
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Job time : 41 secs
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: Patentin version 3.1
SEQ ID NO 692
LENGTH: 15
                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                               4 KSLLYKDGKTYL 15
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4 KNLKIEDSDTYI 15
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US-10-084-813-693
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Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 18, Appl Sequence 11, Appl Sequence 11, Appl Sequence 16, Appl Sequence 3, Appl Sequence 3, Appl Sequence 16, Appl

Sequence Sequence Sequence Sequence

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US-08-159-339A-133
US-08-360-125-23
US-08-450-578-23
US-09-017-628-23
US-09-014-880-23
US-08-450-363-23
US-08-447-960-18
5443956-15
US-08-159-339A-219
US-08-159-339A-219
US-08-159-331-615A-16
US-08-169-16
US-08-073-15
US-08-073-15
US-08-08-16-16
US-08-08-16-16
US-08-16-16
US-07-829-669-16
US-07-829-669-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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93.8%;
                      10004091614051114
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amino acid
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                April 22, 2003, 13:11:19 ; Search time 14 Seconds (without alignments) 33.626 Million cell updates/sec
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Sequence 22,
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Sequence 3
Sequence 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*

1. /cgr2_6/ptodata//iaa/5A_COMB.pep:*

2. /cgr2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgr2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgr2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

5. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

6. /cgr2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-672-345C-25
US-08-672-345C-25
US-09-214-095D-22
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US-09-214-095D-19
US-08-672-345C-19
US-08-672-345C-38
US-09-214-095D-19
US-09-214-095D-19
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US-09-214-095D-19
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
US-08-44-626-4
US-08-44-626-4
US-08-44-626-32
US-08-134-346A-17
US-08-134-346A-17
US-08-134-346A-17
US-08-129-930B-68
US-08-129-930B-68
US-08-50-55BE-29
US-08-50-55BE-29
US-08-50-55BE-29
US-08-64-66-16
US-08-50-55BE-29
US-08-50-55BE-29
US-08-50-55BE-29
US-08-64-62-65
US-08-60-55BE-29
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US-08-60-55BE-29
US-08-60-55BE-29
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 RSSKSLLYKDGKTYLN 16
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Match Length
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ö Gaps . Length 16; Indels OPERATING SYSIEM: PC-LOS/MS-LOS
OPERATING SYSIEM: PC-LOS/MS-LOS
OFFWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMUNICATION INFORMATION:
SEQUENCE CLASSIFICS:
SEQUENCE CLASSIFICS: Sequence 22, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS: Score 77; DB 2; Le Pred. No. 1.3e-06; 1; Mismatches 0;

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Gaps
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
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Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN RELEASE #1.0, Version #1.30
SOFTWARE PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 19:
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT FILICATION NUMBER: US/09/214,095D
CURRENT FILIG DATE: 1999-07-19
NUMBER OF SEQ IN 00S: 121
SOFTWARE: PatentIN version 3.0
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Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper and Dunham Lip
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    ; Sequence 25, Application US/09214095D; Patent No. 6280987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.1%;
93.8%;
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amino acid
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LENGTH: 16 amino acids
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murinae gen. sp
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LENGTH: 16
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                                                                  RESULT 4
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
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Sequence 22, Application US/09214095D

Sequence 22, Application US/09214095D

Parent No. 6280987

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERROR:
CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT APPLICATION NUMBER: US/09/214,095D

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 22

LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION INFORMATION
US-08-672-345C-25
; Sequence 25, Application US/08672345C
; Patent No. 5948650s;
; Patent No. 5948650s;
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
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ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-672-345C-25
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Pred. No. 2.8e-06;
2; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5
These 14; Conservative
   Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-28
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                                                                                      1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                     RESULT 8
US-09-214-095D-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-672-345C-43
                                     Matches
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JOSTON 1976

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.6%;
Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i: 16 amino acids
amino acid
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ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYLN 16
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         RSSKSLLYKDGKTYLN 16
                                           1 RSSRSLLYRDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-672-345C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-214-095D-19
                                                                                                                                                       RESULT 6
US-08-672-345C-28
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92.6%; Score 757; DB 4; Length 16;

Query Match

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Pred. No. 2.8e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/08672345C

Patent No. 548658

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York
Indels
                                                                                                                                                                                                      Sequence 28, Application US/09214095D; Patent No. 6280987; Fatent No. 6280987; GRENRAL INFORMATION:
GRENRAL INFORMATION:
APPLICANT: Landry, Donald; TITLE OF INFORMATION:
FILE REFERENCE: 51400-A-PCT-US; CURRENT APPLICATION NUMBER: US/09/214,095D; CURRENT FILING DATE: 1999-07-19; NUMBER OF SEQ ID NOS: 121; SOFTWARE: Patentin version 3.0; SEQ ID NO 28; LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 24-JUM-1996

CLASSIFICATION: 435

ATTONREY/AGENT INFORMATION:

NAME: White, 10hn P.

REGISTRATION NUMBER: 28,678

REFRENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 100 43:

SEQUENCE CRARACTERISTICS:

LENGTH: 16 aming acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps
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                                                                                                 Score 69; DB 4; Length 16; Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%; Score 69; DB 4; Length 16; 87.5%; Pred. No. 2.7e-05; Live 0; Mismatches 2; Indels
                                                                                                                                        1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-438-123-1
) Sequence 1, Application US/08438123
) Patent No. 5552233
) GENERAL INFORMATION:
) APPLICANT: Lindholm et al
TITLE OF INVENTION:
) TITLE OF INVENTION:
) ADDRESSEE: Lowe, Price, Leblanc & Becker
) CORRESPONDERE Lowe, Price, Leblanc & CITY
) CITY Alexandria
) CITY: Alexandria
) STATE: Virginia
) COUNTRY: USA
                                                                                                                                                                                                                                                                                                                Sequence 79, Application US/09214095D;
Patent No. 6280987;
GENERAL INFORMATION:
APPLICANT: Landry, Donald;
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/214,095D;
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 16
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              Query Match 85.2%;
Best Local Similarity 81.2%;
Matches 13; Conservative
               ; TYPE: PRT
; ORGANISM: Murinae gen. 8p.
US-09-214-095D-43
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Matches 14; Conservative
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ORGANISM: Murinae gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CHAIN
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US-09-214-095D-79
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Pred. No. 2.7e-05;
O; Mismatches 2; Indels
                                     Score 69; DB 2; Length 16;
Pred. No. 2.7e-05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                  Sequence 79. Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/09214095D

| Patent No. 6280987
| GENERAL INFORMATION:
| APPLICANT: Landary Donald
| TITLE OF INVENTION: ANT-COCAINE CATALYTIC ANTIBODY
| FILE REFERENCE: 51400-A-PCT-US
| CURRENT APPLICATION NUMBER: US/09/214,095D
| CURRENT FILING DATE: 1999-07-19
| NUMBER OF, SEQ ID NOS: 121
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York

COUNTRY: USA

ZIP: 10036

ZIP: 10036

COMPUTER: ELABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC COMPATIAN
COMPUTER: TIBM PC COMPATIAN
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIPRACATION: 435

ATTORNEY AGENT INFORMATION:
NAME: White, John P. RECISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
                                   Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative
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                                                                                                                    1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                 1 KSSQSLLYSDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-214-095D-43
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US-08-672-345C-43
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Score 49, DB 1; Length 16;
Pred. No. 0.055;
5; Mismatches 2; Indels
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/24,626
FILING DATE: July 15, 1994
CLASSITICATION: 424
PRIOR APPLICATION NUMBER: PCT/GB92/0251
FILING DATE: December 4, 1992
CLASSITICATION WHERE: PCT/GB92/0251
FILING DATE: December 4, 1992
CLASSITICATION WHERE: PCT/GB92/0251
FILING BATE: Bacember 4, 1992
CLASSITICATION NUMBER: 1808-153A
REGISTRATION NUMBER: 1808-153A
TELECOMMUNICATION INFORMATION:
REFERENCE (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 22, 2003, 13:14:20 Job time : 15 secs
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                               : 16 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.5
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSSKSLLYKDGKTYLN 16
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MOLECULE TYPE: protein
          Washington
                          D. C.
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US-08-244-626-4
i Sequence 4, Application US/08244626
i Fatent No. 5502167.
i GENERAL INFORMATION:
i APPLICANT: Waldmann, Herman
APPLICANT: Lowis, James Scott
APPLICANT: Lowis, Alan Peter
i TILLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
ITILE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 34
i CORRESPONDENCE ADDRESS:
ADDRESSER: S55 Thirteenth Street, N. W.
                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                  Score 55; DB 1; Length 16;
Pred. No. 0.0056;
2; Mismatches 2; Indels
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Pred. No. 0.018;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (1)...(16)
LOCATERION: (1)...(16)
US-09-406-532-18
                                                                                                       LENGTH: 16

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
US-08-438-123-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.2%;
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.3%;
Matches 11; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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April 22, 2003, 13:20:30 ; Search time 43 Seconds (without alignments) 15.650 Million cell updates/sec Run on:

US-09-674-716B-5 31 1 LMSTRAS 7 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

456 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir2: * 4: pir4: * PIR 73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	gene p20K protein	pyruvate kinase (E	dnazx-like protein		ell recept	20% protein - Rick	34.5K structural p	34.5K structural p	serrawettin W2 - S	addrecan - bovine	hypoxanthine phosp	Ig heavy chain CRD	T-cell receptor be		T-cell receptor be	surface protein te	hypothetical prote	parasporal crystal	alpha-1,4-glucan-p	Fc epsilon RIIb -	acetylcholinestera	hypothetical prote		u	URF2 protein - Xan	primase - Citrobac	pap fimbrial requl		u
SUMMARIES	I50412	A11490	40469	151434	PT0518	•	H44817	F44817	A58728	S42620	A37114	PT0295	PT0577	PT0565	PT0700	869237	A37765	S14159	B26206	A46474	A34026	B33541	155382	I78890	870154	140702	B37325	T14910	PT0686
DB 1	:				2						•															~			
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Score	14	13	12	12	12	11	11	11	11	11	10	10	10	. 10	10	10	10	10	10	10	10	10	10	σ	6	σ	თ	σ	თ
	-	8	m	4	2	9	7	80	6	10	11	12	13	14	15		17	18	19	20	21	22	23	24	25	56	27	28	29

T-cell receptor be dnaA protein - Pse hybothetical 6 pro	D-FP2.5 region - m T-cell receptor be T-cell receptor ga	laminin B1 - weste orf 3 rara 5'-regi microcin C7 - Esch	pilE protein - Esc mabinlin II chain seed protein ws-5	<pre>myomodulin - Calif neuromodulatory pe neuromodulatory pe neuromodulatory pe</pre>
2 PT0695 2 B34835 2 PC4127	2 149808 2 PT0643 2 A41946	2 I49421 4 S15596 2 S45311	2 S25266 2 S38516 2 E61491	2 A28340 2 S33244 2 S33245 2 S33246
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29.0 29.0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	29.0 29.0	29.0 29.0	289.0 29.00 29.00
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30 31 32	. w w w w 4 w	3 3 3 3 3 3 3	39 440 11	44 44 44 ሪሃ 62 44 በኒ

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pyruvate kinase (EC 2.7.1.40) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Os-Unn-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
C;Accession: Al1490
R;Hjelmquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
B;cohem. Biophys. Res. Commun. 61, 559-563, 1974
A;Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase ph. A;Reference number: Al1490; MUID:75127438; PMID:4375989
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-6 c4DE>
A;Residues: 1-6 c4DE>
A;Residues: 1-6 c4DE>
A;Residues: glycolysis; phosphotransferase
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20K protein - Rickettsia rickettsii (fragment)
C.Species: Rickettsia rickettsii
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C.Accession: B31836
R.Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia ricke
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C;Species: Leuconostoc oenos phage P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: H44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
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C;Species: Leuconostoc oenos phage P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
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A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4262874
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35.5%; Score 11; DB 2; I
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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3 STRAS
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CiAccession: PT0518
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                         GACCEBBION: 140469

S. Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A;Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.

A;Reference number: 140469

A;Reference number: translated from GB/EMBL/DDBJ

A;Reference processing of Bacillus subtilis small cytoplasmic RNA.

A;Accession: 140469

A;Reference rumber: translated from GB/EMBL/DDBJ

A;Residues preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-5 cRES.

A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204

C;Genetics:
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51434
R;Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nicle: Acids Res. 12, 4939-4958, 1984
A;Title: Are there major developmentally regulated H4 gene classes in Xenopus?.
A;Reference numbor: I51391; MUID:84247348; PMID:6330691
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                                      dnaZX-like protein - Bacillus subtilis (fragment)
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40469
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Pred. No. 2.8e+05;
1; Mismatches 1; Indels
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Pred. No. 2.8e+05;
3; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-6 <WOO>
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: adult thymus, strain BALB/c
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Best Local Similarity 40.0%;
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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Firedeada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j A; Reference number: PT0222; MUID:91108337; PMID:1899102
A; Recession: PT0295
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-5 < YAM>
A; Residues: 1-5 < YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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J. Exp. Med. 114, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0577
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C;bpsciese: Homo sapiens (man)
C;bate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0295
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C;Species: Mns musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0577; PT0574
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Cispecies: Mus musculus (house mouse)
C;bate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0565
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                                                                                 32.3%; Score 10; DB 2; Length 5; llarity 66.7%; Pred. No. 2.8e+05; Conservative 1; Mismatches 0; Indels
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    C;Keywords: glycosyltransferase; pentosyltransferase
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A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
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A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
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C;Species: Serratia marcescens
C;Species: Serratia marcescens
C;Species: Serratia marcescens
C;Date: 10-Feb-1998
E;Accession: A58728
R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
J. Bacteriol. 174, 176, 1792
A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and A;Reference number: A58728; MUID:92193260; PMID:1548227
A;Reference number: A58728
A;Stetus: unencoded polypeptide
A;Molecule type: protein
A;Residues: 1-5 cMAT.
A;Experimental source: strain NS 25
C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocatic C;Reywords: blocked anino end; blocked carboxyl end; D-amino acid; lipoprotein; unencode F;1/Modified site: D-leucine (Jeu) #status experimental
F;4/Modified site: D-phenylalanine (Phe) #status experimental
F;1-5/Cross-link: 3-bydroxydecanoyl amino pdd, ester carboxyl end (Leu-Ile) #status expe
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Cipate: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
Cipate: 28-Jun-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
A; Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
A; Ritle: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Furt
A; Reference number: A37114; MUID:90337955; PMID:2199439
A; Ratures: preliminary
A; Residues: 1-5 < YUA>
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Cipate: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
Cipate: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
Cipatession: $42620
Apritte: Aggrecan in bovine tendon.
Airtle: Aggrecan in bovine tendon.
Aireference number: $42620; MUID:94340214; PMID:7520336
Aireference number: S42620; MUID:94340214; PMID:7520336
Aireference number: S42620
Aireference number: S42620; MUID:94340214; PMID:7520336
Aireference number: S42620
Aireference number: S4262
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T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PT0700
C;Accession: PT0700
R;Reeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Theference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Reture: translation not shown
A;Mesidues: 1-5 cPEE>
A;Experimental source: newborn thymus, strain BALB/C
C;Reywords: T-cell receptor
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Unactional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Reference number: PT0565
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;EES
A;Estatus: 1-5 <FEE>
A;EES
C;Keywords: 1-5 <FEE>
C;Keywords: T-cell receptor
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SEQUENCE FROM N.A.
MEDLINE=89006280; PubMed=2971595;
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ID BIOA_CITFR

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P42561 hirudo medi
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P01162 macrocallis
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                                                                                                                                                                      April 22, 2003, 13:14:25 ; Search time 11 Seconds (without alignments) 26:394 Million cell updates/sec
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                              GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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IGAO DACDE
DOMS PSECH
PFKA ANTEL
BIOB_CITFR
PKT PERAM
PSK DAUCA
TREI PSERO
UNOG CLOPA
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CHOX ALCSP
DOMI_PSECH
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FMRF MACNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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mytilus edu
litoria rub
moniezia ex
locusta mig
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conus imper
mytilus edu
acheta dome
                     mus musculu
                                    oryctolagus
                                                                                                                                           sarcophaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1998) to the SWISS-PROT data bank.
-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-DAN-1990 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxonomanoate aminotransferase
(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrobacter freundii.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                   P13737 r
P82096 ]
P41966 r
P41491 ]
P41495 g
P82158 c
P58803 c
                  P38639
P25154
P13736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X., Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.2%; Score 14; DB 1; Length 7; larity 75.0%; Pred. No. 1.1e+05; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                 ALIGNMENTS
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-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
SWISS-ZDPRAGE; P99025; MOUSE.
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                                                     CIPI_MYTED
CIP2_MYTED
E101_LITRU
FARP_MONEX
LOK1_LOCMI
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CYDPO
CONIM
MYTED
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       NCBI_TaxID=546;
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TISSUE=Liver;
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STANDARD;
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les 2; Conserv
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                                                                                                                                                                      VP19 HS
P23210;
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                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pernollet J.-C., Zlvy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
MAIZE-2DPAGE, P80630; COLEOPTILE.
MaizeDB; 123956; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988)
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                                                                                                                                           oxononanoate = 8-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%; Score 11; DB 1; Length 5; 66.7%; Pred. No. 1.1e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M21222; -; NOT_ANNOTATED_CDS.
InterPro; IPR000954; Aminotran 3.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 5 AA; 582 MW; 6AAABIBIA6F00000 CRC64;
                                                                                                            -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA.
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                                                                                                                                                                                                                                                                                                                 AMINOTRANSFERASES.
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NON TER 5
SEQUENCE 5 AA; 582
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Best Local Similarity
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1 MTT 3
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P80630;
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10 24 MAIZE
10 25 MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91101287; PubMed=1846198;
MEDLINE=91101287; PubMed=1846198;
Flanagan W.M., Papavasailiou A.G., Rice M., Hecht L.B.,
Flanagan M.M., Papavasailiou A.G.,
"Analysis of the herpes simplex virus type 1 promoter controlling the expression of UL38, a true late gene involved in capsid assembly.";
J. Virol. 65.769-786(1991).
-i- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Wistar; TISSUE-Heart;
Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Jungblut P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jungblut P.R.;
Submitted (SEP-1998) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-CEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
TINGTRE
2 OR A.
                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Capsid assembly and DNA maturation protein (Virion protein UL38)
(Capsid protein VP19C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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6 AA.
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UH11 RAT
D UH11 RAT
AC P5576;
DT 15-DEC-199
DT 15-DEC-199
DT 15-DEC-199
DE UNKNOWN DY
OC BUKATYOLA;
OC BUKATYOLA;
OC MAMMALIA;
OC MAMMALIA;
OC ROBERT AND
RN [1]—TAXID
RN [1]—TAXID
RN LI X.-P.,
RA JUMBDUT F
RL SUDMITTEE
CC -1- MISCEI
CT -1- MISCEI
CT -1- MISCEI
CC -1- MISCE
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Gaps

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Indels

RESULT 6 WWA1 ACHFU

Matches

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SEQUENCE.
MEDLINE=87005222; PubMed=3093276;
MORI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-077-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
01-078-1991 (Rel. 17, Last annotation update)
Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
Bacterios faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                   Achatina fulica (Giant African snail).
Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Achatinacea, Achatinidae, Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                             Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
PEBS Lett. 323:104-108(1993).
PIR; S33244; S33244.
Neuropeptide; Amidation.
AMIDATION.
SEQÜENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIRES Lett. 206:69-72 (1986).
-I- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
-I- MISCELLANBOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
SPECIFICITY OF PHEROMONES TO PLASMIDS.
-I- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.8%; Score 8; DB 1; Length 7; ilarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.0%; Score 9; DB 1; Length 7; ilarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                             7 AA.
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                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
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Best Local Similarity
Matches 2; Conserv
Best Local Similarity
Matches 2; Conserva
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ses 2; Conserv
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                                                                                                                                                                         WWA3_ACHFU
P35921;
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SEQUENCE
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P11932;
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                                                                                                                                                                                                                                                                                                                                                              Achatina fulica (Giant African snail).
Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Achatinacea, Achatinidae, Achatina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodilatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108 (1993).
-1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
PIR; $33245; $33245.

NOD RES 7 7 AMIDATION.
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                                                    29.0%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.1e+05; ive 0; Mismatches 1; Indels
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
   7 7 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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Achatina fulica (Giant African snail)
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TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
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MEDLINE=93265912; PubMed=8495720;
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                                                                                            Conservative
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Best Local Similarity
Matches 2; Conservat
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WWA2 ACHFU

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Copper; Metalloenzyme inhibitor.
SEQUENCE 7 AA; 706 MW; 75BBC
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Matches 1; Conserv
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Fidalgo B.V., Najjar V.A.;

Fidalgo B.V., Najjar V.A.;

Fidalgo B.V., Najjar V.A.;

"The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";

Biochemistry 6:3386-3392[1667].

-I. MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE CELL MEMBRANE RELEASES THE ACTIVE PEPTIDE TUTTSIN FROM THE GAMMA CHAIN.

TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avigad G., Markus Z.;
"Idantification of a peptide inhibitor of galactose oxidase from Dactylium dendroides.";
Fed. Proc. 31:447-447(1972).
-!-FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE STALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY BINDING TO ITS PROSTHETIC COPPER GROUP.
PIN; A01341; XEYDGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishioka K., Constantopoulos A., Satch P.S., Najjar V.A., "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin.";
                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1989 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last amotation update)
Galactose oxidase inhibitor.
Dactylium dendroides (Cladobotryum dendroides).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 7; DB 1; Length 4; 50.0%; Pred. No. 1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 47:172-179(1972)
                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phagocytosis-stimulating peptide (Tuftsin)
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MEDLINE=72187087; PubMed=4112769;
                                                                                                                                                                                                              (Rel. 01, Created)
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MIM; 191150; -.
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P06294;
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TUFT_HUMAN
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-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
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Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92028852; PubMed-1681803;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
"Isolation of L.J.-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
novel neuropeptide from sea anemones.";
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group.
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
dehydrogenase subunit S) (CO-DH S) (Fragment).
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                                                 DB 1; Length 7;
1.1e+05;
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75BB01A456D87DB0 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                 Score 7; DB 1;
Pred. No. 1.1e+
2; Mismatches
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llarity 25.0%;
Conservative
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Oxidoreductase; Iron-sulfur.
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MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
"Irranscriptional regulation and gene transcriptional coli, Gene 67:203-211(1988).
                                  McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P., "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Khamide and Antho-Khamide.", Peroc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 6/:2u3-211(1988).
-- CATALYTIC ACTUITY: Dethiobiotin + sulfur = biotin.
--- PATHWAY: Bactin biosynthesis; last step.
--- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
Citrobacter.
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last monotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
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4 AA; 512 MW; 6DD339C9A0000000 CRC64;
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Biotin biosynthesis; Iron-sulfür; Transferase.
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                        MEDLINE=93391436; PubMed=8397415;
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Bukaryota; Mecazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Ilnsecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.

NCBI_TaxID=6978, 6850, 6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-C.maenas;
MEDLINE-86232789; PubMed=2872661;
Stangler J., DickBeen H., Keller R.;
Stangler J., DickBeen H., Keller R.;
"Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=P.americana;
MBDLINE=81225865; PubMed=6113690;
O'Shea M., Adams M.E.;
"Pentapoptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
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Groome J.R., Tillinghast B.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
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                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
      5 AA.
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   PRT;
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   STANDARD;
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PIR; A60411; A60411.
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SEQUENCE 5
PRCT PERAM P01373;
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April 22, 2003, 13:20:00 ; Search time 81 Seconds (without alignments) 17.807 Million cell updates/sec Run on:

US-09-674-716B-5 31 1 LMSTRAS 7 Title: Perfect score: Sequence:

Scoring table:

671580 seqs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

28 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 21:*

Database :

** sp archea:*
** sp archea:*
** sp bacteria:*
** sp fungi:*
** sp fungi:*
** sp invertebrate:*
** sp organelle:*
** sp phage:*
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** sp vertebrate:*
** sp verteb 9. 111: 112: 114: 116: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

# SUMMARIES

			Describtion	P82541 spinacia ol	Q65578 bovine herp	Q47505 escherichia	P70804 azotobacter	Q95945 saccharomyc	P93233 lycopersico	Q99007 hordeum vul	P82181 spinacia ol	P82182 spinacia ol	Q47029 enterobacte	O34028 sphingomona	P83073 bacillus ce	Q15897 homo sapien	Q15903 homo sapien	O99182 gnatholebia	Q63668 rattus norv
SUMMAKIES		;	at	P82541	065578	047505	P70804	095945	P93233	Q99007	P82181	P82182	Q47029	034028	P83073	Q15897	Q15903	099182	063668
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## ALIGNMENTS

RESULT 1

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Rehm B.H.A., Erresvag H., Valla S.,
"A new Azorobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.",
J. Bacteriol. 178:5884-5889(1996).
NON TRR 1
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MEDLINE-81069865; PubMed-6254986;
MEDLINE-81069865; PubMed-6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the micochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase.";
J. Biol. Cham. 255:11927-11941(1980).

EMBL; V00694; CAA24066.1;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
VCBI_TaxID=4932;
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01-FEB-1997 (TYEMBLrel. 02, Created)
01-FEB-1997 (TYEMBLrel. 02, Last sequence update)
01-JUB-2002 (TYEMBLrel. 21, Last annotation update)
Inside intron 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Mitochondrion.
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MEDLINE=96427318; PubMed=8830682;
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01-FEB-1997 (TrEMBLrel. 02, C;
01-FEB-1997 (TrEMBLrel. 02, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
AlgT protein (Fragment).
ALGT.
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MEDLINE=9609297; PubMed=8522520;
GONZALEZ-PROTOT J.E., San Millan J.L., Castilla M.A., Moreno F.;
GONZALEZ-PROTOT J.E., San Millan J.L., Castilla M.A., Moreno F.;
"Structure and organization of plasmid genes required to produce the translation inhibitor microcin C7.";
J. Bacteriol, 177:7131-7140(1995).

EMBL, X57583; CAA40808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia:
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Query Match 35.5%; Score 11; DB 10; Length 6; Best Local Similarity 66.7%; Pred. No. 6.7e+05; Matches 2; Conservative 1; Mismatches 0; Indels
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29.0%; Score 9; DB 2; Length 7;

Best Local Similarity 66.7%; Pred. No. 6.7e+05;

Matches 2; Cohservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Hypothetical 0.8 kDa protein (Fragment).
Bovine herpesvirus 1. no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NUBL TAXID=10320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA; 763 MW; 644DD44861B406F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;
                                                                                                                                                                                                                                                                                                                            7 A.A.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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5 AA; 600 MW; 61E3344DD6F00000 CRC64;

SEQUENCE

7 AA.

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Lycopersicon esculentum (Tomato).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                MEDLINE-97351561; PubMed-9207843; Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; "Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.0%; Score 9; DB 10; Length 7; 50.0%; Pred. No. 6.7e+05; rative 1; Mismatches 1; Indels
                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA; 828 MW; 71B412C7377415D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                            (iycopersicon esculentum).";
Plant Mol. Biol. 34:275-286(1997).
EMBL; U75692; AAC49682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                       PRELIMINARY;
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Best Local Similarity
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4 LVRT 7
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LE-ACS1B.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X54643; CAA38455.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
Calcium; Multigene family.
NON_TER 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
MEDLINE=91329704; PubMed=1831055;
Accobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aleurone layers.";

Plant Mol. Biol. 16:713-721(1991).

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC

LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.

-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

-!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
BARLEY.
                                                                                                                                               Last sequence update)
Last annotation update)
     Ä.
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                                                                                                                                                                                                                                            (Fragment)
                                                                                                 Created)
PRT;
                                                                                            01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
Alpha-amylase (EC 3.2.1.1)
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley)
          PUT THE SECOND CONTRACTOR OF S
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C STRAIN—CV. ALWARO; TISSUE=LEAF;

KX MEDLINE=20435798; PubMed=10874046;

KX Yamaguchi K., Subramanian A.R.;

RT "The plastid ribosomal proteins. Identification of all the proteins in the plastid ribosomal proteins. Identification of all the proteins in RT The 50 S subunit of an organelle ribosome (chloroplast).";

LJ Biol. Chem. 275:2846-28482(2000).

C -: FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOWAL RNA.

CC -: MISCELLUARE LOCATION: CHLOROPLAST.

CC -: MISCELLUARE LOCATION: CHLOROPLAST.

CC -: MISCELLUAREONS NO THE 2D-GEL ITS MW IS: 16.5 KDA.

CC -: MISCELLUAREONS TO THE LIOP PAMILY OF RIBOSOWAL PROTEINS.

CC -: SIMILARLY: BELONGS TO THE LIOP PAMILY OF RIBOSOWAL PROTEINS.

CC -: SIMILARLY: BELONGS TO THE LIOP PAMILY OF RIBOSOWAL PROTEINS.

CC -: SIMILARLY: BELONGS IN BIOSOWAL LIOP PARTIAL.

CO -: SIMILARLY: BELONGS TO THE LIOP PAMILY OF RIBOSOWAL PROTEINS.

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MEDILINE=2043=798; Pubmed=10874046;
Yamaguchi K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 20, Last annotation update)
Chloroplast 50s ribosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spenatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllidae, Caryophyllales, Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spinacia oleracea (Spinach).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Caryophyllidae, Caryophyllales; Chenopodiaceae; Spinacia.

NCBI_TaxID=3562;
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Length 5;
                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last amnotation update)
Chloroplast 508 ribosomal protein L10 beta (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER 6 6 SS21B415B05DB000 CRC64; SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
25.8%; Score 8; DB 10; I 25.0%; Pred. No. 6.7e+05; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA.
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                                                                                  Conservative
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01-JUN-2000
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1 MANK 4
                                                                                                                                                                 2 MSTR 5
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    Query Match
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PR.182
PR.183

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Kim Y.-C.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
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Best Local Similarity
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1 MKDT 4
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5 VNT 7
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P83073
AC P83073;
DT 01-0CT-2
DT 01-0CT-2
DE 88 KDB PO
DE Bacillac
OC Bacillac
OC Bacillac
OC Bacillac
OC Bacillac
NX [1]
RP SEQUENCE
RP SEQ
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Q15897
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MEDLINE=94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-VIa gene encoding a novel 3-N-
acetyltraneferase.";
Antimicrob. Agents Chemother. 37:2074-2079(1993).
BMB112; M88012; AAA16193.1; -.
NON_TER. 1
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047029 PRELIMINARY; PRT; 7 AA.
047029 047029 PRELIMINARY; PRT; 7 AA.
04702916 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Ad Al protein (Fragment).
AD Al.
Enterbacter cloacae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Enterboacter.
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Bacteria, Proteobacteria, alpha subdivision, Sphingomonadaceae, Sphingomona, Proteobacteria, alpha subdivision, Sphingomona, NCBI TaxID=56193, [1] — [1] — [1] — SEQUENCE FROM N.A.
STRANS-D777;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Matches 1; Conserved
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034028
AC 034028;
DT 01-JAN-1DT 01-JAN-1DT 01-DEC-2DE CATECholder CATECHOLDEC-2DE Sphingor OX NCBI TAN NCBI TAN NCBI TAN NCBI TAN SEQUENCE RC STAINELER SEGUENCE RC STAINELER SEGUENCE RC STAINELER SEGUENCE RC STAINELER SEGUENCE STAI
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047029
047029
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TISSUE=PLACENTA;

Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,

Caskey C.T.H.;

Tasolation of chromsome-specific genes by reciprocal probing of

arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

ENBL; L32077; AAA73887.1; -.

NON TER 7 7

SEQÜENCE 7 AA, 814 MW; 672B1DD3372046B0 CRC64;
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(15897).
(1-NOV-1996 (TYEMBLYE). 01, Last sequence update).
(1-NOV-1996 (TYEMBLYE). 01, Last sequence update).
(1-NOV-1996 (TYEMBLYE). 19, Last annotation update).
(1-DEC-2001 (TYEMBLYE). 19, Last annotation update).
(1-NOM-1995 (Human).
(1-NOW-1996 (H
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01-0cr.2001 (TrEMBLrel. 18, Last sequence update)
01-0cr.2001 (TrEMBLrel. 18, Last annotation update)
88 kDa protein (Fragment).
8acillus cereus.
Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
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19.4%; Score 6; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                            Query Match 22.6%; Score 7; DB 2; Length 7; Best Local Similarity 33.3%; Pred. No. 6.7e+05; Matches 1; Conservative 2; Mismatches 0; Indel
Dioxygenase.

NON TER 1 1

SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;
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Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to the SWISS-PROT data bank.
NON TER 5
SRQÜENCE 5 AA; 623 Mw.
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL:

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MEDLINE=20072928; PubMed=10603257;
Murphy W.J., Thomerson J.E., Collier G.E.;
"Phylogeny of the Neotropical killifish family Rivulidae
(Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
                                                                                                                                                                                                                                                                                                                                               (clone XP7E7B) (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
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6.7e+05;
ches 0; Indels
  0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome oxidase I (Fragment).
                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(clone XP7R7B) (Fragment).
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7 AA; 899 MW; 672721F6CB572030 CRC64;
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Pred. No. 6.7e+
1; Mismatches
  1; Mismatches
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EMBL; AF002591; AAD01074.1; -.
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Best Local Similarity 50.0%;
Matches 1; Conservative
  Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQÜENCE
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Matches
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Peptide fused to i MAb 55.1 light cha Hepatitis C virus Tumour antigen ant

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Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain CDR2 of catalytic antibody 6A12.
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                                                                                                                                                                                             AAY08713
AAB079523
AAY95234
AAY35227
AAX32227
AAY0235
AAU70335
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AAN97028
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AAW07065
                                    AAW31179
AAY05016
AAY05016
AAW95283
AAW95223
AAR30157
AAR57966
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AAR57966
AAR50317
AAR60317
AAR6914
AAR94485
AAB35205
AAR46961
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                        AAR76083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW39819 standard; peptide; 7 AA
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 16-JUN-1998 (first entry)
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25-JUN-1997;
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 AAW39819;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAW39876
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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                     100.0%; Score 31; DB 19;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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                                                                                           AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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         in far smaller doses than antibodies that antagonise cocaine by simply binding
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100.0%; Pred. No. 7.8e+05;
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                                                              Claim 13; Page 81; 147pp; English.
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                                                                          Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
Light chain CDR2 of catalytic antibody 12H1.
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This sequence represents complementarity determinating region 2
(CDR L2) of the light chain of murine anti-CD23 (FCERII) monoclonal
antibody Cl1 (see also ANY32262). The invention provides altered
antibodies, such as chimeric or humanised antibodies, which comprise
Sufficient of the amino acid sequences of Cl1 light and heavy chain
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see LANY32254-59) to render them capable of binding to the CD23
CDRs (see CDRS soluble CD23 formation for treatment of arthritis,
lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
clabetes, uvelis, dermatitis, proriasis, urticaria, nephrotic
syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
colitis, Crobn's disease, Sjogren's syndrome, allergies, allergic
asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
eczema, graft-versus-host disease, COPD, insulitis, bronchitis
(particularly chronic bronchitis) or diabetes (particularly type 1
for studying interactions between CD23 and various ligands and
collidetes), and B-cell malignancies (claimed). They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                      CD23; FCBRII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                            urticaria; nephrotic syndrome; glomerulonephritis;
inflammatory bowel disease; ulcerative colitis; Crohn's disease;
joggren's syndrome; allergy; asthma; rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes;
B-cell malignancy; therapy.
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                                                                                                                                                                                                                                                                 Light chain CDR L2 of mouse anti-CD23 MAb C11.
                                                                                                                                          AAY32255 standard; Peptide; 7 AA.
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Best Local Similarity
Matches 7; Conserv
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LMSTRAS
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AAW39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 389, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl occaine. The 389 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 389 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that
                                                                                                                                                                                                                              Variable domain, lambda light chain, catalytic antibody; degradation, cocaine, cocaine transition state analogue; TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.3%; Score 28; DB 19; Length 7; 85.7%; Pred. No. 7.8e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                 Light chain CDR2 of catalytic antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 80; 147pp; English.
                                                                                                       AAW39816 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39876 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US10965.
                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0672345,
                                                                                                                                                                  16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-077166/07.
                                                                                                                                                                                                                                                                              overdose; addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AB;
LMSTRAS 7
                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            simply binding
                             LMSTRAS
                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LMSTRAS
                                                                                                                                                                                                                                                                                                                                            WO9749800-A1
                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Landry DW;
                                                                                                                                     AAW39816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
4
                                                                                                                                                                                                                                                                                                             Mus
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AAW39876
ID AAW3
XX
AC AAW3
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0; Gaps

Conservative

Hein MB;

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02-MAY-2001; 2001WO-US14349
                                                                                                  02-MAY-2000; 2000US-0563222
                                                                                                                        (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                    WPI; 2002-055482/07.
                               WO200183806-A1.
          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2000.
                                                      08-NOV-2001
                                                                                                                                               Hiatt AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY81430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY81430
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW39975-77 represent the sequences of the light chain complementarity determining regions (CDRs) of a catalytic antibody which is capable of degrading occaine. A series of occaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found to have CDRs of the present sequence. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                 Light chain CDR2 of a catalytic antibody capable of degrading cocaine.
                                                     Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                     New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgW; IgG; IgA; IgB; IgB; IgY; IgM; kappa; lambda; CHBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%; Score 27; DB 19; Length 7; 85.7%; Pred. No. 7.8e+05; ive 0; Mismatches 1; Indels
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                                                                                                                                                         /note= "not specified"
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 5; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU70329 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Kappa II light chain CDR2.
                                                                                                                                                                                                                                                                       (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                  96US-0672345.
                                                                                                                                                                                                                             97WO-US10965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
          16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                       overdose; addiction.
                                                                                                                                                                                                                                                                                                                 WPI; 1998-077166/07.
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                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                  25-JUN-1996;
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                                                                                                                                                                                                                             25-JUN-1997;
                                                                                                                                                                                WO9749800-A1
                                                                                                                                                                                                     31-DEC-1997
                                                                                                                                                                                                                                                                                              Landry DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU70329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoslobulin binding protein (198P) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transformed cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoslobulin molecule. The method is useful for preparing an immunoslobulin binding protein carray, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian in IgBP of immunoslobulin derived peptide that may be incorporated into an IgBP of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 7.8e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prugAS vector; Cellulomonas fimi; endoglucanase C; CBD; cellulose binding domain; polysaccharide binding peptide; fusion protein; recombinant protein; cell separation; affinity phase separation.
                                                                                                                                                                                               Disclosure; Page 14; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY81430 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuery Match
Best Local Similarity 71.**,
Similarity 71.**,
Similarity 71.**,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                                                                               preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LMSTRAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| |||
1 LVSNRAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
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AntiнBs; monoclonal antibody; Epstein Barr virus; EBV; adr type; human; HBs antigen; hepatitis C.

Homo sapiens

Peptide Seg ID No:6 of JP11089576.

25-JUN-1999 (first entry)

AAY06840;

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(UYBR-) UNIV BRITISH COLUMBIA
                             WPI; 2000-328038/28.
                                                                                                                                          Query Match
Best Local Similarity
  24-JUL-1996;
         08-APR-1992;
                24-JUL-1995;
              24-MAY-1994
                         наупев СА,
                                                                                                                                      Sequence
                                                                                                                                  rector
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The invention relates to a novel two-phase partition system for affinity separation which comprises a phase-forming oligosaccharide polymer to which a polyseccharide binding peptide (PBP) binds, and a phase to which a polyseccharide binding peptide (PBP) binds, and a phase to separation inducing agent. The system may be used for the separation and purification of recombinant proteins from cell cultures. The protein of interest is expressed in the host cell as a fusion protein with a conformation system. The fusion protein partitions into the polysaccharide binding peptide, and the cell lysate or fermentation of interest is expressed in the host cell as a fusion protein with a conjopaccharide bounds to the phase separation system. The fusion protein partitions into the cultose polymer polymer phase, and can then be isolated e.g., via the custom bromide. If the fusion protein has been emplaced such that there is a solution with a low ionic strength, high pl or containing a chaotropic agent, or by the use of chemical cleavage agents such as cransported as the cleaved from the PBP, which remains bound to the oligosaccharide. Proteins that may be purified using the method of the invention include a wide variety of medically and industrially important proteins e.g., interlexin 2, interlexin 3, interlexin 2, interlexin 2, interlexin 2, interlexin 2, interlexin 2, interlexin 2, interlexin 3, interlexi
Two-phase partition affinity separation system useful for separating and purifying proteins comprises a phase-forming oligosaccharide polymer and a phase-separation agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ļ
                                                                                                                                                                                                                              Disclosure; Fig 3A; 46pp; English.
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Gaps

The invention relates to an antiHBs monoclonal antibody having the following properties: (A) CDR-3 of H chain variable region; (B) it contains no Epstein Barr virus (EBV); (C) it binds at least one adr type among human HBs antigens. The antiHBs monoclonal antibody is high in antibody titer and has low risk of EBV contamination. It can be used to prevent hepatitis C.

Anti-HBs monoclonal antibody - produced without the risk of Epstein

97JP-0255705. 97JP-0255705.

19-SEP-1997; 19-SEP-1997;

36-APR-1999.

Kilburn DG

Tomme P,

92US-0865095. 90US-0603987. 94US-0249037. 95US-0505860.

96US-0685808 88US-0216794 (NISN ) NISSHINBO IND INC.

WPI; 1999-281053/24.

Claim 4; Page 7; 12pp; Japanese.

Barr virus contamination

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Tumour antigen; antibody; CDR; complementarity determining region; binding molecule identification; tumour-specific binding polypeptide; cancer therapy; light chain.
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                      Tumour antigen antibody light chain CDR2 clone F14.
                                                                                                                                                                                                                              Score 19; DB 20; L. Pred. No. 7.8e+05; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                  AAY05015 standard; peptide; 7 AA.
                                                                                                                                                                                                                               61.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0905825.
97US-1112222.
                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US16280.
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                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                     Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              (IXSY-) IXSYS INC.
                                                                                                                                                                                                                   7 AA;
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                04-AUG-1998;
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04-AUG-1997;
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3 STRAT
                                                                                                                                                                                                                                                        3 STRAS
                                                                                                                                                                                                                                                                                                               AAY05015;
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                       RESULT 10
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61.3%; Score 19; DB 21; Length 4; 100.0%; Pred. No. 7.88+05; rive 0; Mismatches 0; Indels

4; Conservative

Matches

2 MSTR 5

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AAY06840 standard; peptide; 7 AA.

RESULT 9
AAY06840
ID AAY0

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The present invention describes a method for detecting a retroviral genetic recombinant having agg and pol functions, involving a cell suspected of having a recombinant and propagating the recombinant in the presence of any necessary helper functions. This is useful as it enables the detection of vectors which are able to replicate in the host cell, and allows the production of vectors suitable for gene therapy. The present sequence is a peptide fragment used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence may be fused to the haemagglutinin 2 (HA2) fragment (amino acids 66-222) of influenza A and the resulting fusion protein used in a vaccine. The purpose of this particular sequence is not given in the specification although such additional peptides to the virus antigen may contain another influenza antigen or other antigen or confer some advantage upon expression of the HA2 peptide. Alternatively the fusion peptide may comprise a sequence which is selectively cleavable by a proteolytic enzyme or upon exposure to a
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide; influenza; vaccine; virus; antigen; expression; cleavage;
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                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide fused to influenza A polypeptide for use in vaccine.
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                                                                                                                                                                                                                                                       Score 18; DB 22; Length 6;
Pred. No. 7.8e+05;
0; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shatzman A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 45; 58pp; English.
Example 5; Fig 14; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR46961 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                           58.1%;
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-118165/14.
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les 4; Conserv
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                                                                                                                                                                                                                     6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein.
                                                                                                                                                                                                                                                                                                                                      2 MSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                                            1 MGARAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                          This sequence represents a light chain complementarity determining region (CDR) from a tumour antigen specific antibody.

The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising: (a) selectively immobilising a diverse population of binding molecules to a solid support; (b) simultaneously contacting the diverse population immobilised on the solid support with 2 or more Ifgands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as targeting agents for cancer therapy that minimises impact on non-tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroviral recombination assays, systems and cells, useful for evaluating the risk of producing a replication-competent retrovirus from a retroviral-based vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroviral recombination assay; gene therapy vector; viral vector; gag; pol; replication; HIV.
                                                                        Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two or more ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 20; Length 7;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviral recombination assay peptide fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB35205 standard; Peptide; 6 AA.
                                                                                                                                                                            Claim 15; Page 57; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cappes JC, Wu X, Wakeield J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.3%;
80.0%;
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Huse WD, Watkins JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                    WPI; 1999-153951/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA;
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Tumour antigen, antibody, CDR, complementarity determining region; binding molecule identification; tumour-specific binding polypeptide; cancer therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                         AAW31170-W31181 are peptides derived from various gentoypes of hepatitis C virus. The peptides were used for the production of PCR (polymerase chain reaction) primers used for discrimination between hepatitis C virus (HCV) genotypes. Classification of the genotype of HCV can be achieved precisely and simply according to the international Standardisation of Classification. The primers can be used to distinguish between HCV genotypes la, lb, 2a, 2b, 3a, 3b, 4, 5a, 6a and 6b.
                                                                                                                                                                                                                                                                             Primers used for determining hepatitis C virus genotype - rapid and accurate method of hepatitis C virus genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.1%; Score 18; DB 18; Length 7; 57.1%; Pred. No. 7.8e+05; without 2; Indels
   3b; 4; 5a; 6a; 6b; diagnosis; amplification; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour antigen antibody light chain CDR2 clone F15.
                                                                                                                                                                                                                                                                                                                                Example 1; Page 18; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05016 standard; peptide; 7 AA.
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                                                                                                                                 96JP-0038875.
                                                                                                                                                                95JP-0352511.
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97US-1112222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153951/13.
N-PSDB; AAX28193.
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                                   Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                                                                                                                                                               (SRLS-) SRL KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LMSTRAS 7
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1 LLSPRGS
                                                                 JP09234072-A.
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04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                 01-FEB-1996;
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01-FEB-1995;
                                                                                                 09-SEP-1997,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy and light chains of MAD 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CAS55.1. It is optionally humanized and in the form F(ab)?, F(ab)', Far, FV, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody: immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; genotype determination; la; lb; 2a; 2b; 3a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus genotype 5a peptide, OMM25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 97; 121pp; English.
                                                                                                             AAR76083 standard; Peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                          humanized antibody; immunotoxin
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                                                                                                                                                                             (first entry
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Rose MS, Wright AF;
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Best Local Similarity
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LMSTRA 6
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LTSTRS 7
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03-DEC-1993;
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Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two or more ligands

Claim 15; Page 57; 80pp; English.

This sequence represents a light chain complementarity determining region (CDR) from a tumour antigen specific antibody.

The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising: (a) selectively immobilising a diverse population of binding molecules to a solid immobilising a diverse population of binding molecules to a solid on the solid support with 2 or more ligands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as transpiring agents for cancer therapy that minimises impact on non-tumour tissues. 

7 AA; Sequence

Gaps ö Query Match
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels

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13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	7A-30 Sequence 30, Appl	Segmence 32.	Sequence 10.		Sequence 11.	3 Sequence 43.	Seguence 46.	Sequence 8. A	Sequence 11.		Sequence 19.	Semience 53. A	Seguence 58.	Sequence 62.	Semience 75.	Sequence 17.	Semience 45.		( )
	£	TI	US-09-977-797A-30	US-09-977-797A-3	US-10-146-305	US-09-249-011A-18	US-10-144-644-11	US-09-828-708-43	US-09-828-708-46	US-09-947-137-8	US-10-078-458-11	US-09-800-433-8	US-10-014-77	US-09-995-973	US-10-116-255-58	US-09-913-238	US-09-850-351A-75	US-09-839-497A-17	US-09-828-708-45	US-09-828-708-47	04 000 000 00
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Sequence 49, Appl Sequence 82, Appl Sequence 7, Appli Sequence 63, Appli	Sequence 56, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 22, Appl Sequence 66, Appl	12, A 07, Ap 71, Ap	29, 71, 78, 102	Sequence 87, Appl Sequence 87, Appl Sequence 15, Appl Sequence 30, Appl Sequence 36, Appl
	9 US-09-B88-B82A-66 9 US-09-925-179-35 10 US-09-802-077-35 10 US-09-802-096-35 10 US-09-736-959A-22 10 US-09-990-782-6	9 US-09-977-797A-82 9 US-09-967-237-107 9 US-10-217-957-3 9 US-10-217-957-4 10 US-09-765-086-71 10 US-09-765-086-71	10 US-09-947-137-29 10 US-09-220-220-71 10 US-09-839-447A-78 10 US-09-782-980-102 10 US-09-405-499-3	ъ.
15 14 14 14 45.2 14 45.2 15 15 15 15 15 15 15 15 15 15 15 15 15	14 45.2 14 45.2 14 45.2 14 45.2 14 45.2 6 15 75.2 6	14 45.2 7 1 14 45.2 7 1 14 45.2 7 1 14 45.2 7 1 14 45.2 7 7 1 4 45.2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	14 45.2 13 41.9 13 41.9 4 13 41.9 4	13 41.9 4 1.3 41.9 44.13 41.9 61.9 64.19 64.19 64.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 65.19 6
888	42 22 22 24 44 44 44 44 44 44 44 44 44 4	0 m m m m	. W W W W 4 4	1 4 4 4 4 1 0 6 4 8

#### ALIGNMENTS

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Sequence 30, Application US/0997797A

Publication No. US20030044772A1

GENERAL INFORMATION:

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Wu, Herren

TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

TITLE OF INVENTION: NUMBER: US/09/977,797A

CURRENT APPLICATION NUMBER: US/09/977,797A

CURRENT APPLICATION NUMBER: 09/129,026

PRIOR PILING DATE: 1998-08-04

PRIOR PLING DATE: 1998-08-04

PRIOR FLING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 136

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09977797A
Publication No. US20030044772A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserva
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US-09-977-797A-30
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US-09-977-797A-32
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Gaps

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FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized

OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-249-011A-18
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 54.8%; Score 17; DB 9; Length 7; Best Local Similarity 80.0%; Pred. No. 2.7e+05; Matches 4; Conservative 0; Mismatches 1; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPER: RIOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FLING DATE: 2002-08-08
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: US 08/363131
FILING DATE: 20-DW-1995
ATTORNEY/AGENT INFORMATION:
NAME: SULTON 1996
ATTORNEY/AGENT INFORMATION:
NAME: SULTON JOFFER 3-1094
ATTORNEY/AGENT INFORMATION:
NAME: SULTON JOFFER 3-1094
ATTORNEY/AGENT INFORMATION:
TELEPONER: 610-270-5024
TELEPONER: 610-270-5024
    CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELBEAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Patent No. US2002013035A1
GENERAL INFORMATION:
APPLICANT: VURAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REPERENCE: OV1740
CURRENT APPLICATION NUMBER: US/10/146,305
CURRENT PILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR PILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: KOPATENTI I.71
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APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
FILE REFERENCE: 08702.0081-00000
                                                                                                                                                                                                                                                                                                                                                             Gaps
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Sest Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1;
FILE REFERENCE: AME-06805
CURRENT APPLICATION NUMBER: US/09/977,797A
CURRENT FILING DATE: 2002-06-25
FRIOR APPLICATION NUMBER: 09/129,026
FRIOR APPLICATION NUMBER: 08/904
FRIOR FILING DATE: 1998-04
FRIOR FILING DATE: 1997-08-04
SOFTWARE: PATENT NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09249011A
Patent No. US20020176855A1
GENERAL INFORMATION:
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APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARRENO, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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KNIGHT, ANDREA
O'HARA, DENISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10
                                                                                                                                                                                                                            TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-32
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US-10-146-305-10
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APPLICANT:
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US-10-078-458-11
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                                                                                    Sequence 8, Application US/09947137; Sequence 8, Application US/09947137; Satent No. US20020137023A1
; GENERAL INPORMATION:
; APPLICANT: Smith, Bruce F.;
; APPLICANT: Samoilova, Tatiana
; TITLE OF INVENTION: Methods and Compositions for Targeting;
; TITLE OF INVENTION: Compounds to Muscle
; FILE REFERENCE: 5721-8
; CURRENT FILING DATE: 2001-09-05
; PRIOR PILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%; Score 16; DB 10; Length 7; 60.0%; Pred. No. 2.7e+05; tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Phage display library peptides US-09-947-137-8
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US-10-078-458-11
Sequence 11, Application US/10078458
PUblication No. US2002018734A1
GENERAL INFORMATION:
APPLICANT: COTTON, Rohald
TITLE OF INVENTION: PEPTIDE DERIVATIVES
CURRENT APPLICATION WUMBER: US/10/078,458
CURRENT APPLICATION NUMBER: US/09/308,175
FRIOR APPLICATION NUMBER: US/09/308,175
FRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
SRQI PRIOR FILING DATE: 1997-11-21
SRQI PRIOR FILING DATE: 1996-11-27
SRQI PRIOR FILING DATE: 1996-11-27
SRQI PRIOR PRIOR DATE: 1996-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0°
Matches 3; Conservative
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1 MSTQS 5
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APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Burton, D.
APPLICANT: Schaler, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
TITLE OF INVENTION: autoimmune disease
TITLE OF INVENTION: autoimmune disease
TITLE OF INVENTION: UNDER: US/09/828,708
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application US/09828708
Patent No. US/00201467531
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particifitz BEFERENCE: 1361.005USI
TITLE OF INVENTION: Autoimmune disease
TITLE REFERENCE: 1361.005USI
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                   54.8%; Score 17; DB 9; Length 7; 80.0%; Pred. No. 2.7e+05;
                                                                                                                                                                               1; Indels
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80.0%; Pred. No. 2.7e+05;
tive 0; Mismatches 1;
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Patent No. US20020146753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
COGANISM: Homo sapiens
US-09-828-708-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-43
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Matches 4; Conserv
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                                                                        ; MOLECULE TY
US-10-144-644-11
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US-09-828-708-43
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TYPE: PRT ORGANISM: Artificial Sequence
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US-09-800-433-8
; Sequence 8, Application US/09800433
; Sequence 8, Application US/09800433
; Patent No. US20020106378A1
; GENERAL INFORMATION:
; APPLICANT: O'Hare and Elliott
; TITLE OF INVENTION: Materials and methods for intracellular transport and
; TITLE OF INVENTION: their uses
; TITLE OF INVENTION UNMER: US/09/800,433
; CURRENT APPLICATION NUMBER: US/09/800,433
; CURRENT PILING DATE: 1990-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFFWARE: Patentin Ver. 2.0
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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FREERING US/202099173A1

GENERAL INFORMATION:

APPLICANT: D'AZZO, Alessandra

APPLICANT: Bonglovanni, Antonella

APPLICANT: Donglovanni, Antonella

APPLICANT: Nastasi, Tommaso

TITLE OF INVENTION: Proctein Specific for Cardiac and Skeletal Muscle

FILE REPERBUCE: 2427/1F509-US1

CURRENT APPLICATION NUMBER: US/10/014,774

CURRENT FILING DATE: 2001-10-29

FRIOR APPLICATION NUMBER: PCT/US00/11900

FRIOR APPLICATION NUMBER: PCT/US00/11900

FRIOR APPLICATION NUMBER: DCT/US00/11900

FRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 3.0

FROM TOWER TO SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: peptide US-09-800-433-8
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48.4%; Score 15; DB 12; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 48.4%; Score 15; DB 10; Length 6; Best Local Similarity 75.0%; Pred. No. 2.7e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: CHOO, Yen
TITLE OF, INVENTION:
FILE REFERENCE: 8325-2003 / G7-USI
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-774-19
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US-10-014-774-19
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CURRENT APPLICATION NUMBER: US/95,973

CURRENT PLING DATE: 200-03-19

SOFTWARE PERMONE: Exemination of Artificial Sequence: zinc finger

SOFTWARE PARENT DATE: 2.0

SOFTWARE PERMONE: Parent Number 1.0

SOFTWARE PERMONE: Parent Number 1.0

SOFTWARE PERMONE: Parent Number 1.0

GRANIBM ARTHITICAL STATEMENT NUMBER: SOFTWARE 1.0

PERMONE: SOFTWARE 1.0

A TASS 1.0

A TASS 4.0

Macches 31.0

A TASS 4.0

Macches 33.0

A TASS 4.0

Macches 34.0

Macches 35.0

Macches 36.0

Macches 36.
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Gaps

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Score 15; DB 10; Length 7; Pred. No. 2.7e+05; 1; Mismatches 0; Indels

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TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-850-351A-75
                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 22, 2003, 13:29:09 Job time : 16 secs
                               LENGTH: 7 amino acids
                                                     TYPE: amino acid
STRANDEDNESS: single
       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. USSQU201010080Alel Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
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COUNTRY: US

COUNTRY: US

ZIP: 32606-669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATIOR SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                      Query Match 48.4%; Score 15; DB 9; Length 7; Best Local Similarity 60.0%; Pred. No. 2.7e+05; Matches 3; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gaineaville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INPORMATION:
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Feitelson, Jerald S.
Schnepf, H. Brnest
Narva, Kenneth B.
Stockhoff, Brian A.
Schmeits, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75, Application US/09850351A Patent No. US20020100080A1 GENERAL INFORMATION:
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 75:
                                                                                                                                                                                                                                                             FEATURE:

OTHER INFORMATION: Synthesized
US-09-913-238-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PIEM PC compatible
COMPUTER: PARTABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PARTABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING BATE: 24-UUN-1996
CLASSIFICATION NUMBER: 18,06/672,345C
FILING BATE: 24-UUN-1996
CLASSIFICATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 0575/51400
TELEDEHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08672345C
Patent No. 5948658
GENERAL INFOATION:
APPLICANT: Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDESS:
ADDRESSEE: Cooper and Dunham LLP
PCT-US93-08435-24
PCT-US93-08435-37
PCT-US93-08435-41
PCT-US93-08435-41
US-08-503-062-14
US-08-503-062-14
US-09-084-605B-8
US-09-084-605B-8
US-09-084-605B-8
PCT-US96-11495-14
US-09-175-14
US-09-082-358B-47
PCT-US96-11495-14
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-08-064-111C-10
US-08-064-11C-10
US-08-064-11C-10
US-08-064-11C-10
US-09-012-126-8
US-09-012-126-8
US-09-012-126-8
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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Best Local Similarity
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     Best Loca
Matches
     RESULT
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                                                                                                               April 22, 2003, 13:21:20 ; Search time 28 Seconds (without alignments) 7.356 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-08-672-345C-26

US-08-672-345C-26

US-09-214-095D-23

US-09-214-095D-26

US-09-214-095D-26

US-09-214-095D-26

US-09-214-095D-20

US-09-214-095D-20

US-08-672-345C-80

US-08-672-345C-80

US-08-672-345C-80

US-08-672-345C-80

US-08-672-345C-80

US-08-672-345C-80

US-08-672-345C-80

US-08-125-20

US-09-011-628-20

US-09-011-628-20

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US-08-637-647-11
US-07-987-264-5
US-08-450-363-20
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                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
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31
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Match Length
                               Copyright
                                                                                                                                                                                                                    1 LMSTRAS
                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 7
                                                                                                                                                                                                  Perfect score:
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Maximum DB
                                                                                 OM protein
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                                                                                                                                                                                                                                                                                                                                      Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
**WINDER OF SEQ ID NOS: 121
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Patent No. 6280987
GENERAL INFORMATION:
APPLICATE LANGTY, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FULE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 2; I
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
      NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-378-0400
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn version 3.0
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Best Local Similarity 100.0
....has 7; Conservative
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ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: FRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-26
                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-672-345C-29
                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LMSTRAS 7
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US-09-214-095D-26
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US-08-672-345C-26

Sequence 26, Application US/08672345C

Parent No. 5948658

GENERAL INFORMATION:
TILLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
; CORRESPONDER, ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; STREET: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-UN-1996
CLASSIFICATION: 1996
CLASSIFICATION: TOPPOTER: US/678
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION: TOPPORMATION:
TELECOMMUNICATION INCRMATION:
TELEFRAX: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAC COMPATIBLE
COMPUTER: APENDED
COMPUTER: IBM PC compatible
COMPUTER: APENDED
SOFTWARE: PACENTIN Release #1.0, Version #1.30
SOFTWARE: APENICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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85.7%; Pred. No. 1.9e+05;
tive 1; Mismatches 0; Indels
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; Sequence 80, Application US/08672345C
; Pattent No. 5948658
; Pattent No. 5948658
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                Sequence 20, Application US/09214095D; Patent No. 6280987; GRNERAL INFORMATION: APPLICANT: Landry, Donald; TITLE OF INVENTOR: 51400-A-PCT-US; CURRENT FAPLICATION NUMBER: US/09/214,095D; CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0; SEQ ID NO 20; SEQ ID NO 20; LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIP: 10036
COMPUTER REAABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 8, 678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPAX: 212-278-0400
TELEPAX: 212-391-0525
INPORMATION FOR EQ. IDNO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
murns: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 4; Pred. No. 1.9e+05; 1; Mismatches 0
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-20
                       6; Conservative
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  Best Local Similarity
                                                            1 LMSTRAS 7
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                       Matches
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Sequence 20, Application US/08672345C

Sequence 20, Application US/08672345C

Patent No. 594865B

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                      RESULT 6
US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent NO. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TILLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FLUE REFERENCE: 51400-A-PCT-US
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 29
; SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:

ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PARENTEN RC-BOS/MS-DOS
SOCTWARE: PARENT NUMBER: US/08/672,345C
PILING DATE: 24-UNN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 31; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0;
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LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Murinae gen. sp
US-09-214-095D-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LMSTRAS 7
      LMSTRAS 7
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                                             1 LMSTRAS
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Gaps
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SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
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US-08-505-860C-9

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REFERENCE/DOCKET NUMBER: CBDT.017.01US;
TELECOMMUNICATION INFORMATION:
TELEFPONS: (650) 328-4400
TELEFPAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/ACENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CEDT.017.00US
TELECOMUNICATION:
TELECOMUNICATION:
(650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: no
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Best Local Similarity
-Loca 4; Conserva
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Fatent No. 6048715
GENERAL INFORMATION:
APPLICANT ATMES, CHARLES A., et al
TITLE OF INVENTION:
NUMBER OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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NAME/KEY: CHAIN
LOCATION: (6)..(6)
COTHER INFORMATION: X at position 6 represents any amino acid
US-09-214-095D-80
                                                             87.1%; Score 27; DB 2; Length 7;
85.7%; Pred. No. 1.9e+05;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                           US-09-14-095D-80

Sequence 80, Application US/09214095D

Patent No. 62809N1

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-CCCAINE CATALYTIC ANTIBODY

FILE REPRESENCE: 51400-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT PILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPIET : USA

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/685,808
FILING DATE: 24-JULY-1996
CLASSIFICATION: 435
RECORRENT NUMBER: 08/505,860
FILING DATE: 24-JULY-1995
ATTORNEY/AGENT INPOWMATION:
NAME: REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27; DB 4; I Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.1%; Score 27; DB Best Local Similarity 85.7%; Pred. No. 1.9e Matches 6; Conservative 0; Mismatches
                                                             Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Murinae gen.sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LMSTRAS 7
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                                                                                                                                                                               1 LMSTRAS 7
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         US-08-672-345C-80
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US-08-685-808-9
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LENGTH: 7
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(416) 868-1482
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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
نامع 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MSTRAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | | | 2
2 LSYRAS 7
              TELEPHONE:
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Sequence 25, Application US/08264093
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Ridout & Maybee
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFWWARE: ASCII Editor
CURRENT APPLICATION DATA:
FILING DATE:
FILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                 APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-UNN-1994
INFORMATION POR SEQ ID NO: 31.
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

"LENGTH: 7 amino acids
"LENGTH: 7 amino acids
"LENGTH: 7 amino acids
"LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%; Score 18; DB 1; Length 7; 80.0%; Pred. No. 1.9e+05; ive 0; Mismatches 1; Indels
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PRIOR APPLICATION DATA: No. 5639863 applicable ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
                         Sequence 31, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Then 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 STRAS 7
US-08-353-400-31
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Gaps
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APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: McMillan, Ecombinant ILS Antagonists Useful in TITLE OF INVENTION: Treatment of ILS Mediated Disorders NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: SmithKline Beecham Corp./Corporate STREET: P. O. Box 1539-UW2220
CITY: King of Prussia
STREET: Pennsylvania
                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                     Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 1; Length 7; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elegapy disk
COMPUTER: Elegapy disk
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
SCOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
TLING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/363131
FILING DATE: 13-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTATION NUMBER: 950282
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               54.8%; Score 17; DB 1; I 66.7%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 11, Application US/08467420A; Patent No. 5683892
                                                                                                     TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.8%;
80.0%;
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO:
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Matches	8	4,	4; Conservative			0; Mismatches	1,	1; Indels 0; Gaps	0,	Gaps	0
ò	m	3 STRAS 7									
q _Q	m -	STRES	7								
Search c Job time	in o	pletec 29 BE	Search completed: April 22, 2003, 13:25:06 Job time : 29 secs	1003, 1	13:	25:06					

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 13:28:56 ; Search time 14 Seconds (without alignments) 61.801 Million cell updates/sec Run on:

US-09-674-716B-7 48 Title: Perfect score:

1 QQLVEYPFT 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

789

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		dip			SOLVENING	ST THE	
Result No.	Score	Query	Query Match Length	DB	. QI		Description
				-			
-	21	43.8	σ	N	S66635		alpha-2-macroglobu
7	19	39.6	ιn	~	E60274		major protein anti
e	16	33.3	e	m	A43391		TRH-like tripeptid
4	14	29.5	4	~	A32039		tyrosine-melanocyt
ស	14	29.5	4	7	PT0240		Ig heavy chain CRD
9	14	29.5	2	7	PQ0009		angiotensin-conver
7	14	29.5	9	~	JN0861		peptidyl-dipeptida
80	14	29.5	7	٦	A61324		dermorphin - Rohde
თ	14	29.2	7	~	836662		
10	14	29.5	7	7	821230		_
11	14	29.5	7	7	842620		aggrecan - bovine
12	14	29.2	Φ	N	S66646		cardioacceleratory
13	14	29.5	6	N	A61620		locustamyotropin I
14	14	29.5	6	N	B49712		ATP-binding protei
15	13	27.1	D.	N	JS0319		subesophageal gang
16	13	27.1	ø	~	A61049		halo-toxin - Pseud
17	13	27.1	9	~	151317		bHLH transcription
18	13	27.1	7	7	E33932		Ig mu chain D regi
19	13	27.1	7	~	PX0008		glucuronosyltransf
20	13	27.1	7	4	156695		hypothetical L2 pr
21	13	27.1	80	~	S16324		w
22	13	27.1	σ	~	S15850		vitamin D3 26-mono
23	13	27.1	O.	0	A61358		bradykinin-like pe
24	13	27.1	σ	0	A61057		Thr-6 bradykinin -
25	13	27.1	o.	~	A26744		bradykinin-like pe
26	13	27.1	6	~	A61363		bradykinin - commo
27	13	27.1	σ	7	A60579		bradykinin-like pe
28	13	27.1	o.	~	A26363		
29	13	27.1	σ	7	839766		cardioactive pepti

cardioactive pepti bradykinin - horn	60K Ca binding pro Ig heavy chain CRD enamelin i - bovin	growth hormone rec cardioactive pepti hydroxyproline-3-b	pap fimbrial regul phytosulfokine alp pilE protein - Esc	amine oxidase (cop capsid protein VP- neuropeptide calla	neuropeptide calla serum albumin - do
9 2 S27233 9 2 S65433	9 2 PT0080 9 2 PT0285 9 2 S10784	9 2 I46023 9 2 S39767 9 2 A43065	5 2 B37325 5 3 JT0870 7 2 S25266	7 2 A38081 8 2 PL0184 8 2 D47393	8 2 E47393 8 2 B45800
13 27.1 13 27.1	13 27.1 13 27.1 13 27.1	13 27.1 13 27.1 13 27.1	12 25.0 12 25.0 12 25.0	12 25.0 12 25.0 12 25.0	12 25.0 12 25.0
30 31	3 3 3 3 4 4	35 37	38 39 40	4 4 4 4 4 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4	44

#### ALIGNMENTS

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CjAccession: S66635
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrn
R;Dolmer, X.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrn
R;ESS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66635
A;Accession: S66635
A;Accession: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.8%; Score 21; DB 2; Length 9; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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3 EFPF 6
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major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Immun. 59, 372-382, 1991
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Accession: E60274
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 39.6%; Score 19; DB 2; Length 5; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels

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Gaps

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A43391 TRH-like tripeptide - alfalfa C;Species: Medicago sativa (alfalfa) 6 YPFT 9 2 YPIT RESULT 3 ઠે g

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peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
(Species: Sarda orientalis (striped bonito)
(C)Species: Sarda orientalis (striped bonito)
(C)Accession: JN0861
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Blotechnol. Biochem. S7, 1743-1744, 1993
A;Title: Isolation and characterization of anglotensin I-converting enzyme inhibitory pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Experimental source: liver C; Comment: The carboxyl end is essential for the protein's expression of angiòtensin I-c C; Superfamily: bradykinin-potentiating peptide C; Keywords: angiotensin-converting enzyme inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actions.

Action Comparison of Series (1994)

C. Species Payllomedusa rohdal (Rohde's leaf frog)

C. Species Phyllomedusa rohdal (Rohde's leaf frog)

C. Dete: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C. Accession: A61324 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C. Accession: A61324 #sequence_revision of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz A; Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz A; Reference number: A61324; MUID:82029915; PMID:7287302

A; Residual type: protein

A; Residual: 1-A00N3

C; Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

C; Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin F; C/Modified site: 1-Alpdroxyproline (Pro) (partial) #status experimental

F; 7/Modified site: amidated carboxyl end (Ser) #status experimental
                                                                                                                                    angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N.Alternate names: ficus latex peptide 2
S.Species: Ficus carica (common fig)
C.Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C.Accession: P00009
R.Maruyama, S.; Miyoshi, S.; Tanaka, H.
A.Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A.ATitle: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A.ACcession: P00009
A.Reference number: P00008
A.Residues: 1-5 - ARR.
A.Residues: 1-5 - ARR.
A.Residues: 1-5 - ARR.
A.Experimental source: latex
C.Keywords: angiotensin-converting enzyme inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.2%; Score 14; DB 2; Length ilarity 100.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 0; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-6 < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JN0861
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3 YP 4
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Matches
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Matches
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
R;Laccession: A43391
B;Laccession: A43391
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391; MUID:92388092; PMID:1517203
A;Mescession: A43391
A;Molecule type: protein
A;Molecule type: protein
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A3203y
R;Horvath, A.; Kastin, A.J.
R;Horvath, Chem. 264, 2115-2119, 1989
A;Tible: Chem. 264, 2115-2119, 1989
A;Tible: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Reference number: A32039; MUID:89123285; PMID:2563371
A;Reference number: A32039
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C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
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C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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ilarity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0;
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Matches 2; Conserv
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Matches 2; Conserv
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1 QYP 3
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ATP-binding protein p46 - dog (fragment)

Cispecies: Canis lugus familiaris (dog)

Cispecies: Canis lugus familiaris (dog)

Ciscession: B49712

Ciscession: B49712

Ciscession: B49712

Ciscession: A10: Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.

J. Biol. Chem. 269, 1744-1749, 1994

A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap A;Reference number: A49712; MUID:94124514; PMID:8294423

A;Status: preliminary
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Affilte: Isolation, identification and synthesis of locustamyotropin III and IV, two add A; Reference number: A61620
A; Accession: A61620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C)Accession: S66646

K; Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.

FEBS. Lett. 371, 311-314, 1995

A; Title: Anino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the tA; Reference number: 866646; MUID:96013159; PMID:7556618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: A61620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardioacceleratory protein 2b - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
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A;Molecule type: protein
A;Residues: 1.9 <26CH>
C;Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Leu) #status experimental
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                                          29.2%; Score 14; DB 2; L4 conservative 0; Migmatch.
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Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1;
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Best Local Similarity 33...
Best Local Similarity 2; Conservative
                              Query Match
Best Local Similarity
2, Conserva
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-8 <HUE>
C, Keywords: cartilage
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                                                                                                                                                                                                                                                                                                                                                                                               dermorphin (Lys-7) [validated] - two-colored leaf frog
G:Species: Phyllomedusa bicolor (two-colored leaf frog)
G:Species: Phyllomedusa bicolor (two-colored leaf frog)
G:Species: Do-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
G:Accession: 836662
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G.; Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G.; Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, L.; Falconieri Brapamer, G: Kreil, G: Kreil, G.
R:Mignogna, G: Severini, C.; Simmaco, M.; Negri, G: Kreil, G: Kreil
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R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Miller. 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of A;Reference number: S21152; MulD:92339502; PMID:1633846
A;Reference number: S21230
A;Reference pression s21230
A;Reference pression s21230
A;Reference number: S21230
A;Reference number: S21230
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
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29.2%; Score 14; DB 1; Length 7;
larity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0; Indels
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R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggrecan in bovine tendon.
A;Reference number: 842620; MUD:94340214; PMID:7520336
A;Accession: 842650
A;Molecule type: protein
A;Residues: 1-7 <VOG>
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Query Match
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Matches 2; Conserv
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S42620
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Gaps

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subsophageal ganglion pentapeptide - house cricket
CiSpecias: Acheta domesticus (house cricket)
CiSpecias: Acheta domesticus (house cricket)
CiSpecias: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
CiAccession: JS0319
Riwicker, C.; Wicker, C.
Comp. Bloochem. Physiol. C 88, 185-187, 1987
A/Itle: Isolation and structure of a peptide isolated from the suboesophageal ganglion A/Reference number: JS0319
A/Accession: JS0319
A/Accession: JS0319
A/Residues: 1-5 <WIC>
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29.2%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A,Molecule type: protein
A,Residues: 1-9 <NIG>
C,Keywords: ATP; endoplasmic reticulum; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 22, 2003, 13:31:56 Job time : 14 secs
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JS0319
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

Run on:

April 22, 2003, 13:25:11 ; Search time 24 Seconds (without alignments) 15.554 Million cell updates/sec

US-09-674-716B-7 48 1 QQLVEYPFT 9 Perfect score:

Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

231 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

		Description	Q10582 bothrops ja	P30096 homo sapien	159 treponema h	P81820 carcinus ma	carcinu	locue	homo sa		achet						P40929 homo sapien		ä		P81805 carcinus ma	.806 carcinus ma		~	_	P31890 ascaris suu	1815 carcinus ma	_	P81821 carcinus ma	4	0	Ŋ	_	156 cydia pom	1809 carcinus ma
		Dea	010	P30	P8015	P81	P8181	P41	P30	P30	P15	P41	<b>P</b> 81	P82	P82	P38	<b>P4</b> 0	<b>P8</b> 1	<b>P</b> 58	P82	P81	P81	P81	P81	P8.	<u>13</u>	<b>P8</b>	P81	P8.	P8.	P41	P8.	P4.	P8.	P81
SUMMARIES		ΠD	ANG2 BOTJA		FLA2_TREHY			LMT3_LOCMI	UPA3_HUMAN	UPA7_HUMAN	SUGA_ACHDO	FAR1	0N0	PPK		SS	UHA2_HUMAN	AL14_CARMA		ASPZ_LACSN		ALL3	ALL4	ALLS	ALL7	FAR2		. AL15_CARMA	AL18 CARMA	ALL3_CYDPO		1	-	- 1	ALL7_CARMA
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		Score	15	15	15	14	14	14	14	14	13	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
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P81811 carcinus ma P81812 carcinus ma	P22396 locusta mig P81813 carcinus ma	P80975 thunnus obe P04277 homo sapien	P82072 litoria rub P01151 sus scrofa	P82071 litoria rub P82073 litoria rub		
1 ALL9 CARMA 1 ALL9 CARMA	1 LMT2_LOCMI 1 AL10_CARMA	1 COXE_THUOB 1 NEUX_HUMAN	1 RE31_LITRU 1 THYL_PIG	1 RE21_LITRU	1 AKH_TABAT	
	12 25.0 8 12 25.0 9		11.5 24.0 S 11 22.9 3			
3.4 3.5	36			44 44 C3 E4	44.45	

### ALIGNMENTS

RESULT 1 ANG2 BOTJA STANDARD; PRT; 8 AA.  AC 010582; DT ANG2 BOTJA STANDARD; PRT; 8 AA.  DT 01-OCT-1996 (Rel. 34, Last sequence update) DT 01-OCT-1996 (Rel. 37, Last annotation update) DT 01-OCT-1996 (Rel. 37, Last annotation update) DE Angiotenain-like peptide II (Fragment). DE Angiotenain-like peptide II (Fragment). DE Capidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; CO Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; CO Viperidae; Crotalinae; Bothrops.  NCBI TaxID=8724; RN NCBI TaxID=8724; RN NCBILE=5620832; PubMed=8829801; RN MEDILE=5620832; PubMed=8829801; RN MEDILES-5620832; PubMed=8829801; RN MEDILES-5620832; PubMed=8829801; RN MEDILES-5620832; PubMed=8829801; RN MEDILES-5620832; PubMed=8829801; RN Webconstrictor; Plasma; Serpin. DR ROSOCONSTRICTOR: Plasma; Serpin. RN Vasoconstrictor; Plasma; Serpin. RN Vasoconstrictor; Plasma; Serpin. RN Vasoconstrictor; Plasma; Serpin. RN Vasoconstrictor; Plasma; Serpin. BR ROSITE; PSOUS44; SERPINF, PARTIAL. KW Vasoconstrictor; Plasma; Serpin. BR ROSITE; PSOUS44; SERPINF, PARTIAL. AUSOCONSTRICTOR: 8 AA; 1046 MW; DDD761E0482D40A CRC64; AUSOCONSTRICTOR 8 AA; 1046 MW; DDD761E0482D40A CRC64; AUSOCONSTRICTO

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TOPAA HUMAN STANDARD; PRT; 8 AA.
P30036;
P30036;
D1-APR-1993 (Rel. 25, Created)
D1-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. RESULT 2
UDAA_HUMAN
ID UPAA_HUMAN
ID 10 1-APR
DT 10-APR
DT 16-OCT
DE UMANOW
OS EUKATY
OC BAMMAN
OC MAMMAN
IN [1]
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RN FR SEQUEN
RC TISSUE
RC MADLIN
RC HODE
RC RADLIN
RC RADLIN
RA HUGHE
RA HUGHE
RA HOCHE
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SEQUENCE.
TISSUE=Plasma;
MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;

Gaps

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1; Indels Length 8;

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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Plecyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
                                                                                                                             "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANISMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN PAMILY.
MOD RES

MAIdation; Multigene family.
MAIDATION (POTENTIAL).
SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
        Malacostraca, Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Erachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and identification of multiple neuropeptides of the allacostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:77-734 (1997).
-1- FUNCTION: MAX ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
9 AMIDATION.
SEQUENCE 9 AA; 927 MW; 832D79CDCB46D861 CRC64;
                                                                                                     Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cerebral ganglion, and Thoracic ganglion, MEDLINE-98121193; PubMed-9461295;
                                                                           TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                                                                                                                           Score 14; DB 1; I
Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 50.0%; Score 14; DB 1; I Similarity 50.0%; Pred. No. 1.1e+05; 2; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Locustamyotropin 3 (LOM-MT-3).
Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                                                                                                                                                                9 AA.
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NCBI_TaxID=6759;
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P41489;
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LMT3_LOCM1
1D _LMT3_LV
AC P41489
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JD AL17_CARMA

STANDARD; PRT; 8 AA.

AC P81870;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Caronus maenas (Common shore crab) (Green crab).

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
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                                                                                                                                                                                                                                                                                                                                                                                                       Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetales; Brachyspiraceae; Brachyspira
NCBI_TaxID=159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 1129 MW; 855A19C68B4772D1 CRC64;
                                                                                                             8 AA; 909 MW; 86677B59D1A72042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLAB3 (32 kDa).
-1- SUBCELLULAR LOCATION: PERIPLASH (37 kDa),
-1- SUBCELLULAR LOCATION: Periplasmic flagellum.
UNSURE.
                                                                                                   /FTId=VAR_000004.
                                                                                                                                                                                                                                                                                                             9 AA.
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1 ETVPYMF 7
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P80159;
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01-FEB-1995 (
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ID FAR1 H
AC P41871
DT 01-NOV
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                                                                                                                                                                        "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family.";

Insect Biochem. Mol. Biol. 22:447-452(1992).

-:- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Caelifera,
Acridomorpha, Acridoidea, Acrididae, Oedipodinae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.6, ITS MW IS: 46 KDa.
SWISS-2DPAGE; P30089; HUMAN.
                                                                                                                             Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OGP-1993 (Rel. 25, Last annotation update)
16-OGP-2001 (Rel. 40, Last annotation update)
16-OGP-2001 (Rel. 40, Last annotation update)
16-OGP-2001 (Rel. 40, Last annotation update)
16-OGP-2001 (Rel. 40)
16-OGP-2001 (Graman)
16-OGP-2001 (Gram)
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MEDLINE=93002937; PubMed=1459097;
MEDLINE=93002937; Paquet N., Ravier F., Pasquali C., Sanchez G.J., Frutiger S., Paquet N., Bjellqvist B., Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 1.1e+05;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                MOD RÈS 9 9 AMIDATION.
SEQÜENCE 9 AA, 1140 MW; D5AE1772C9D776C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
                                                                                                                                                                                                                                                                           (MYOTROPIC ACTIVITY).

-!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

InterPro., IPROOL1484; Pyrokinin.

PROSTITE; PS00539; PYROKININ; 1.

Neuropeptide; Amidation; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         h 29.2%;
Similarity 50.0%;
2; Conservative
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                                                                                                    SEQUENCE, AND SYNTHESIS.
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
                                                           NCBI TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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UPA7_HUMAN
ID _UPA7_HUMAN
AC P30093;
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4 FPXT 7
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2 00PF
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NON TER
SEQUENCE
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UPA3_HUMAN
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Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Ensifera,
Gryllidae, Gryllinae, Acheta.
NCBI_TaxID=6997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                    "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714 (1992).
-!- MISCELLANBOUGS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
SWISS-2DPAGE; P30093; HUMAN.
                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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"Isolation and structure of a peptide isolated from the suboesophageal ganglion of Acheta domesticus (orthoptera)."; Comp. Biochem. Physiol. 88c:185-187(1987).
-i- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                             TISSUE-Plasma;
MEDLINE-93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 13; DB 1; Length 5; 100.0%; Pred. No. 1.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.2%; Score 14; DB 1; Length 9; llarity 50.0%; Pred. No. 1.1e+05; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;
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GANGLIA.

PIR, JS0319, JS0319.

GROHENCE 5 AA; 476 MW; 69D76DDDDDDDD0000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Suboesophageal ganglion pentapeptide.
Acheta domesticus (House crickel).
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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Best Local Similarity
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tes 2; Conserv
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01-NOV-1995
01-NOV-1995
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5 EXPY 8
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SEQUENCE
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16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
Periplaneta americana (American cockroach).
Bukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Orthopteroidea; Dictyoptera; Blattcidea; Blattcidea; Periplaneta.
                                                                                                               TISSUE=Corpora cardiaca;
MEDLINE=97353923; PubMed=9210163;
Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
"Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";
Peptides 18:473-478(1997).
                                                                                                     SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6978;
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3 PF
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                                                                                                            Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M., "FWRFamide-related peptides from the kidney of the snail, Helisoma
            Helisoma trivolvis (Snail).

Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Planorbidae; Helisoma.

NCBL TaxID=27815;
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                              Peptides 15:31-36(1994).
-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of needles (N141) (Fragment).
Plub pinaster (Maritime pine).
Bukaryota, Viridiplantee, Stroptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C., "Separation and characterization of needle and xylem maritime pin
                                                                                                                                                                    THE KIDNEY, MANTLE AND SKIN.
-1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
-1- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
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larity 100.0%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Score 13; DB 1; Length 7;
Pred. No. 1.1e+05;
                                                                                                                                                                                                                                  7 7 AMIDATION.
7 AA; 851 MW; 69D40729D76AA810 CRC64;
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100.0%; Pred. No. 1...
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(Rel. 40, Last sequence update)
       PMRFamide-like neuropeptide GDPFLRF-amide,
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
TISSUB=Needle;
MEDLINE=99274088; PubMed=10344291;
                                                                                   TISSUE=Kidney;
MEDLINE=94286417; PubMed=7912428;
TISSUE=Kidney;
                                                                                                                                                                                                                     Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                           Conservative
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ID PPK2_PERAM
AC P82892;
DT 16-0CT-2001 (
                                                                                                                                   trivolvis."
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UNO6_PINPS
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TISSUE SPECIFICITY.
MEDLINE=20189894; PubMed=10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexapoda;
Blattaria;
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MEDLINE=20189894; PubMed=10723010;

Predel R., Eckert M.;

"Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";

J. Comp. Neurol. 419:352-363(2000).

-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUB-Retrocerebral complex;
MEDILINE-99212469; PubMed=10196736;
Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede
"Differential distribution of pyrokinin-isoforms in cerebral and
abdominal neurohemal organs of the American cockroach.";
Insect Blochem. Mol. 18101. 29:139-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                      the American cockroach.";
J. Comp. Neurol. 419:352-363(2000).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Periplaneta americana (American cockroach).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera;
Blattoidea; Blattidae; Periplaneta.
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                                                                                                                                                                                                            (MYOTROPIC ACTIVITY).

-1- TISSUE SPECIFICITY: CORPORA CARDIACA.
-1- MASS SPECTROMETRY: WHE BB3; WETHOD=MALDI.
-1- STHILARLIY: BELONGS TO THE PYROKININ FAMILY.
INTERPRO; IPR001484; PYTOKININ.
PROSITE; PS00539; PYROKININ; FALSE NEG.
Neuropeptide; Amidation; Pyrokinin.
NOD RES
SEQÜENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.1%; Score 13; DB 1; Le llarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Pea-PK-3) (FXPRL-amide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA.
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-1- TISSUE SPECIFICITY: CORPORA CARDIACA.
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9 AA.

PRT;

STANDARD;

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result 15
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                                                                                                                                                                                                                                                                                                                       Carcinus maenas (Common shore crab) (Green crab),
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
Spodoptera eridania (Southern armyworm).
Eukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
NCBI_TaxID=6759, 7130, 7067, 37547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and identification of a cardioactive peptide from Tenebrio
                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=C.maenas; TISSUE=Pericardial organs; Stangier J., Hilbich C., Beyreuther K., Keller R.; "Unusual cardioactive peptide (CCAP) from pericardial organs of the Shore crab Carcinus maenas."; Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=M.sexta;
MEDLINE=33050243; PubMed=1426284;
Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
"Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
FEBS Lett. 313:165-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molitor and Spodoptera eridania.";
Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
-!- FUNCTION: THE BFPECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
-!- TISSUE SPECITICITY: STORED IN PERICARDIAL ORGANS AND RELEASED INTO THE HEMOLYMPH.
PIR; A26363; A26363.
PIR; S27233; S27233.
Neuropeptide; Amidation.
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                                                                                    27.1%; Score 13; DB 1; Length 8; 100.0%; Pred. No. 1.18+05; Live 0; Mismatches 0; Indels
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27.1%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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-1- MASS SPECTROMETRY: WW=996.5; METHOD=WALDI.
-1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
Neuropeptide; Amidation; Pyrokinin.
MOD RES
SRQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 9 AMIDATION.
9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;
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                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
Cardioactive peptide (CCAP).
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MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 15:1459-1465(1994).
-!- MISCELLANEOUS: ON THE 2D-CEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
NON TER
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
01-PEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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Job time : 24 secs
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099187 caloglossa
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09040 momo sapien
09003 bomo sapien
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0811 bos taurus
0811 bos taurus
081059 bombina ori
081059 bombina var
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STRAIN=V2785;
Wyvold C., Birkelund S., Christiansen G.;
The Mycoplasma hominis P120 membrane protein gene contains a 659 base pair hypervariable domain.";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U22025; AAA67455.1; -.
caloglossa
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NCBI_TaxID=2098;
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01-NOV-1996 (TrEMBLrel. 01,
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P120 (Fragment).
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TISSUE=PLACENTA;
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Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antiljarum, a keystone herbivore on
Caribbean reefs.";
                                         Mitochondrion.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoidea; Diadematacea; Diadematoida; Diadematidae;
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O'Hanlon P.C., Briese D.T.;
O'Hanlon P.C., Briese D.T.;
Weydence for hierarchical and non-hierarchical evolution in the Carduinae thistles.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF129846; AAF78138.1; -.
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                                                                                                                STRAIN=DCA3;
MEDLINE=2132337; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
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Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels
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EMBL: AY012858; AAL33832.2; -
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SEQUENCE 9 AA; 1115 MW; EDFBDB1B173B46CA CRC64;
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Last sequence update)
Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Cytochrome oxidase subunit II (Fragment).
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8 AA; 788 MW; 457451B5A76DDB10 CRC64;
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                                Diadema antillarum.
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                                                                                    NCBI_TaxID=105358;
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     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GAP-3, GTPBAS-activating protein (Fragment).
Bos taurus (Bovine).
ENARYOTATI Metasoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                            "The purification of a Rapl GTPase-activating protein from bovine brain cycosol."; J. Biol. Chem. 267:1546-1553(1992).
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Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and Commid libraries.";
Hum. Nol. Genet. 0:0-0(1995).
EMBL; L32078; AAA73888.1; -.
ENNL; ER 1 1
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SEQÜENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(clone XP6AllB) (Fragment).
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MEDLINE=92112868; PubMed=1309786;
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Q14277
ID Q1427
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SEQUENCE FROM N.A.
STRAIN=G66; TRANSPOSON=TN5037;
Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
Nikiforov V.G.;
"Th5037, a Th21-like mercury resistance transposon from Thiobacillus
ferrooxidans.";
Russ. J. Genet. 37:972-975(2001).
Russ. J. Genet. 37:972-975(2001).
RUSS. AJS51743; CAC69252.1; -.
RON TER
SEQÜENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;
                                                                                                                                                                                     Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Torovirus.
NCBI_TaxID=11156;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=90080137; PubMed=2293666;

Snijder E.J., Horzinek M.C., Spaan W.J.M.;

Snijder E.J., Horzinek M.C., Spaan W.J.M.;

A 3'-coterminal nested set of independently transcribed mRNAs is generated during Berne virus replication.";

J. Virol. 64:331-338(1990).

EMBL; M33502; AAA42817.1; -.

NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
NCBL_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Score 14; DB 2; Length 8; Similarity 100.0%; Pred. No. 6.7e+05; 2; Conservative 0; Mismatches 0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Uricase (EC 1.7.3.3) (Urate oxidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 9 AA; 1234 MW; D8EE736B5451AB19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                  Created)
Last sequence update)
Last annotation update)
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llarity 66.7%; Pred. No. 6.7e+05;
Conservative 1; Mismatches 0;
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                                         9 AA.
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01-DEC-2001 (TEMBLrel. 19, Last seq
01-DEC-2001 (TEMBLrel. 19, Last ann
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                                           PRT;
                                                                                  01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 09,
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                                         PRELIMINARY;
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les 2; Conserv
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                                                                                                                                                        ORF3 (Fragment)
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01-MAR-2001
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O934S4;
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Q65711;
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P82858
ID P82858
AC P82858
DT 01-MAD
DT 01-MAD
DT 01-TAD
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RESULT 8
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MEDLINE=94366753; PubMed=8084609; Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T., Bocciardi R., Nijven H., Bolino A., Seri M., Ronchetto P., Pasini B., Bozzano M., Buys C., Romeo G., "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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MEDLINE=21250995; PubMed=11352571;
Nakabayashi K., Scherer S.W.;
Nakabayashi K., Scherer S.W.;

"The human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb
DNA at chromosome 7q35.";

Genomics 73:108-112 (2001).

EMBL; AF318295; AAK49906.1; -.

NON TER 9 9
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94071887; PubMed=7902707;
Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
Takahashi M., Romeo G.;
"Exon structure and flanking intronic sequences of the human RET
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 1 1 1
SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;
                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RET protein short form (Fragment).
                                                                                                                                                                                                                                                                                                                                    proto-oncogene.";
Biochem. Biophys. Res. Commun. 196:1288-1295(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contactin-associated protein 2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the ret proto-oncogene.";
Oncogene 9:3025-3029(1994).
EMBL; Ull532; AAC50102.1; -.
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                                                                                                                Homo sapiens (Human).
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nes 3; Conserv
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RESULT 7 Q96T78

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STRAIN=991614;
Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
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MEDLINE=92218434; PubMed=1560006;
Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
Kato K., Shinohara H., Goto S., Inaguma Y., Morishita B., Asano T.;
"Copurification of small heat shock protein with alpha B crystallin from human skeletal muscle.";
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Chloroplast.
Eukaryota, Rhodophyta, Florideophyceae, Ceramiales, Delesseriaceae,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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                                                                                                                                                                                                                           "Recovery of HIV-1 pol gene sequences by direct sequencing of amplification products derived from plasma samples.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF347459; AAX32535.1; -.
1 1
SEQUENCE 8 AA; 845 MW; 72CDDB1DD736CAE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.2%; Score 14; DB 15; Length 8; Best Local Similarity 75.0%; Pred. No. 6.7e+05; Matches 3; Conservative 0; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 21, Last annotation update)
28 kDa heat shock protein homolog fragment 1 (Fragment).
Homo sapiens (Human).
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Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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NON TER 1 1 1
NON TER 9 9
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Q9UC36
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STRAIN=F-I/RGM;
Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
Mabit DQ52 and DH Gene Rearrangements in Early B-cell Development.";
MOI. Immunol. 0:0-0(1996).
EMBL; U62585; AAB18735.1; -.
NON_TER B 8
SEQUENCE 8 AA; 845 WW; SCA861B5AB58677B CRC64;
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                 Puccinia recondita f. sp. triseti.
Eukaryota; Pungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
Uredinales; Pucciniaceae; Puccinia.
                                                                                                                                                   SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
TISSUE-SPORE;
Aguilar M., Montalbini P., Fineda M.;
Submitted (NOV-2000) to the SWISS--ROT data bank.
-1- PUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXXISOURATE + H(2)O(2) (5-HYDROXXISOURATE DECOMPOSE TO FORM ALLANTOIN).
-!- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: GERMINATION.
-!- SIMILARITY: BELONGS TO THE URICASE FAMILY.
Interpre, IPROGOG42; Uricase.
PROSITE; PSO0366; URICASE; PARTIAL.
Oxidoreductase; Purine metabolism; Peroxisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Q98YK9;
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
G1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
G1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUL.
POL.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Germline DH (Df) gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 8 a 77 MW; 98CladD735B9D76D CRC64; SEQÜENCE 8 AA; 777 MW; 98CladD735B9D76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 66.7
nes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                               NCBI_TaxID=142679;
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Q98YK9
ID Q98YK
AC Q98YK
DT 01-JU
DT 01-JU
DT C1-JU
DT C1-JU
GN POL.
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EMBL; AB023384; BAA88918.1; -.
                                  Kamiya M., West J.A., Zuccarello G.C., Kawai H.;
"Caloglossa intermedia sp. nov. (Delesseriacese, Rhodophyta),
morphologically intermediate between C. leprieurii and C. monosticha,
from the western Atlantic coast.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB030266, BAA90253.1;
EMBL, AB030264; BAA90251.1;
EMBL, AB030265; BAA90259.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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O9TJ85,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment).
STRAIN=SOUTH CAROLINA USA, NEW JERSEY USA, AND GEORGIA USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

29.2%; Score 14; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels
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Similarity 75.0%; Pred. No. 6.7e+05;
3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                Chloroplast. 1 1 SEQUENCE 9 AA, 977 WW; CA1A4DC1B771AB02 CRC64;
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SEQUENCE 9 AA; 977 MW; CALA4DC1B771AB02 CRC64;
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Best Local Similarity
Matches 3; Conserv
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1D 097488
AC 097488
DT 01-MAN
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Search completed: April 22, 2003, 13:31:37 Job time : 30 secs

2 VETP 5

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(without alignments)
16.428 Million cell updates/sec
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::_/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.
GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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48
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult Š

Light chain CDR L3 Light chain CDR3 o Light chain CDR3 o Murine 13H10 light C242:11 MAb kappa Complementary dete Humanised antibody VEGF antagonist an Anti-human CD154 a Complementarity de Description AAR30450 AAY97234 AAE13142 AAB82708 AAB82896 AAW39823 AAW39817 AAY92171 AAY32256 ü 四 Length Query Match 100.0 0.00.00.00.00.00 Score 

99WO-GB01434. 98GB-0009839.

07-MAY-1999; 09-MAY-1998;

18-NOV-1999

(GLAX ) GLAXO GROUP LTD

graft-versus-host disease; B-cell malignancy; therapy

Mus musculus. WO9958679-A1.

		31	64.	ø	σ	23	Ą	AAU74411		Light chain comple
		30	62.	2	σ	19	Ā	AAW59175		PAF re
		30	N	rs	σ	13	Z	AAW39820		chain
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		D 0	n c	<b>,</b>	ט כ	7 :	₹;	W/31/1		or light cha
		o a	n a	<b>~</b> ) (*	ס ע	٦ <u>۲</u>	<b>4</b> 2	WEDI46		Light chain CDK3 p
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		28	m	m	0	21	A	Y82342		Humanised anti-CD1
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		27	w	7	œ	14	Ā	R35879		Hepatitis C virus
		27	S	2	œ	14	Ā	R35880		Hepatitis C virus
		27	S	~	œ	14	Ā	R35878		Hepatitis C virus
		27	6	0	σ,	18	¥.	W23435		CDR-3 of rWI2 ligh
		27	o o	2 (	σ (	13	2	W39877		Light chain CDR3 o
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		, 4	0 <	<b>4</b> C	ט ני	7 6	2 2	262510		Aumanised Fab Vers
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		26	54	N	-	18	A	W01800		Heptapeptide which
		26	4	0	7	20	2	Y42565		Oligopeptide compo
		26	4	~	7	22	2	U79894		Anti-stress agent
		26	◂	7	7	23	Z	U98728		Peptide inhibitor
		26	4	7	æ	17	Z	R97350		Peptide fragment o
		56	4	7	80	18	Ā	AAW30320		Haemorphin peptide
		56	4	7.	σ	17	Z	AAR97349		Peptide fragment o
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XX	AAY32256									
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占3	15-FEB-2000	2000	IJ	(first entry)	entı	<u> </u>				
<b>설</b>	Light c	chain	S	CDR L3 o	Ę.	1186	ant	1-CD23	of mouse anti-CD23 MAb C11.	
X			j	ì	!	) ) 5	Š	1		
¥.	CD23; F	CERII		gE re	cept	or;	DE .	oclonal	CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse	mouse;
Ž 5	MONOCIC	nala	<u>.</u>	body;	5 5	mer	C G	ntiboay	', humanised anti	.body;
¥ 3	complem inflamm	entar	: :3	, dete	rmir	ing.	reg	ion; CL	R; autoimmune di	,
<u> </u>	Hashimoto's thyroiditis; diabet	to'8	. E	roidi	tis	di.	abet	erytue es; uve	iupus eryinematosus; murripie diabetes; uveitis; dermatitis	e scretosis; s; psoriasis;
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<u> </u>	Sjogren	887	g.	syndrome; allerg	allergy	rgy	; ag	thma; r	asthma; rhinitis; eczema;	insulit
Z Z	graft-versus-host B-cell malignancy,	ersu: malig	nar	oer an icy; t	nsease; therapy		2	COPD; bronchitis;	nitis; diabetes;	

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                                                                                                                                                                                                                                                                                                        This sequence represents complementarity determinating region 3 (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal antibodies, such as chimeric or humanised antibodies, which comprise unfibodies, such as chimeric or humanised antibodies, which comprise unfibodies, such as chimeric or humanised antibodies, which comprise unfibodies acreamed to the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haemacopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, colitis, crohn's disease, sportasis, uritaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulergic stathma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cochim; agraft-versus-host disease, COPD, insulitis, bronchitis asthma, interactions between CD23 and various ligands and element of the reddying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                         Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
   Rapson NT,
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Bonnefoy JMP, Crowe SJ, Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW39823 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                        Claim 1; Page 40; 81pp; English.
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Best Local Similarity
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                                                                                           N-PSDB; AAZ34741
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determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of release 3H-benzola catalytic antibodies were identified by their capacity to release 3H-benzola caid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
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                                                                                   AAW39821-23 represent the sequences of the light chain complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable domain, lambda light chain, catalytic antibody; degradation, cocaine, cocaine transition state analogue; TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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smaller doses than antibodies that antagonise cocaine binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain CDR3 of catalytic antibody 3B9.
                                                                                                                                                                                                                                                                                      concentration that can be achieved).
                                                    Claim 15; Page 82; 147pp; English.
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88.9%;
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Best Local Similarity
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                                                                                                                            06-MAY-1993
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                                                                                                                                                                                                                                         Synthetic.
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 identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a gubject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                   Light chain, variable region; complementarity determining region; CDR 3; anti-Tie2 kinase receptor; monoclonal antibody; 15BB; angiogenetic; vascular-general; proliferative; antibohemic; cerebroprotective; cardiant; agonist; antibody inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
                                                                                                                                        Gaps
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                                                                                                             Score 36; DB 19; Length 9;
Pred. No. 7.8e+05;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                   AAY92171 standard; Peptide; 9 AA
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                                                                                                             75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                      Kappa; chain; heavy; complementarity determining region; CDR; MAb; monoclonal antibody; C242:II; murine; IgG; hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
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Pred. No. 7.8e+05;
1; Mismatches 1
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                                                                                                                                AAR30450 standard; peptide; 9 AA.
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ilarity 75.0%;
Conservative
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Best Local Similarity
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QHLEYPFT
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Gaps ö

1; Mismatches

2 QLVEYPFT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothalial growth factors (VEGF). The antibodies neutralise CKDR activation. The immunoglobulin may be a multivalent single chain antibody, a diabody, a triabody, a diabody, a chimarised antibody a diabody, a triabody, a humanised antibody or a chimerised antibody, a diabody, a triabody in molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and ALDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphCcytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibody murine light chain hypervariable region (VL) CDR3.
VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 50; 55pp; English.
                                                                                                                                                                                                                                                                                                    99US-0240736.
                                                                                                                                                                                                                                                28-JAN-2000; 2000WO-US02180
                                                                                                                                                                                                                                                                                     99US-0117726
                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          Zhu Z, Witte L;
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                                                                                                                                                                            WO200044777-A1.
                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                   29-JAN-1999;
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                                                                                                                                                                                                               03-AUG-2000.
                                                                                                                                            Synthetic.
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Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -

(IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC. 31-MAR-2000; 2000US-0540770. 30-MAR-2001; 2001WO-US10504.

WPI; 2001-662942/76. N-PSDB; AAD21668.

Witte L, Rafii S;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-3 used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.6%; Score 31; DB 22; Length 9; 66.7%; Pred. No. 7.8e+05; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF antagonist antibody IMC-1C11 VL CDR-3.
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                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 15; 68pp; English.
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antibody to human CD154 for use

Schuler W;

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sprue, glomerulonephritis, Grave's disease, Hashimoto's thyroiditis, demonytric disease of the newborn, Keratitis, multiple sclerosis, polymyositis, psoriasis, rheumatic fever, rheumatoid atthritis, sarcoidosis, syphilis, tuberculosis, ulcerative colitis,
                                                                                                                                                                                                                                                           CD154 binding molecule, in particular antibody to human CD154 for in treatment, prevention of autoimmune, inflammatory diseases, atherosclerosis, Alzheimer's disease and prevention of transplant
                                                                                                                              (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 23; 37pp; English.
                                                      14-MAR-2001; 2001WO-EP02875.
                                                                                           16-MAR-2000; 2000GB-0006398
                                                                                                                                                                                                                         WPI; 2001-590062/66.
                                                                                                                                                                                    Di Padova FE,
                 20-SEP-2001
                                                                                                                                                                                                                                                                                                                       rejection
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                                                                                                                                                                                                                                                                      condition (e.g.
                                                                                                                                                                                                                                                                              Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 7.88+05;
3; Indels
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                                                                                                                                                (SUNN-) SUNNYBROOK HEALTH SCI (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                      29-JAN-2001; 2001WO-US02839.
                                                                                           28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
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                                                                                                                                                                                                                                                                                                                                        chemotherapeutic agent
                                                                                                                                                                                                                                             WPI; 2001-514531/56.
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                 02-AUG-2001
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                                                                                                                         Gaps
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                                                                                                                         ;
0
                                                                          64.6%; Score 31; DB 22; Length 9; 66.7%; Pred. No. 7.8e+05; ive 0; Mismatches 3; Indels
HIV infection, leukaemia or lymphoma.
                                                                                                                                                                                                                                                                                                               AAG63993 standard, peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2001 (first entry)
                                                                                                                           Conservative
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                  1 QQLVEYPFT 9
                                       9 AA;
                                                                                                                                                                                                        1 QQYNSYPFT
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                                         Sequence
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WO200168860-A1

RESULT 9 AAB8289(

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24-MAY-2000; 2000US-206749P. (IMCL-) IMCLONE SYSTEMS INC.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel monoclonal antibody specific for human sialoadhesin factor-2 for diagnosis, prevention, treatment of allergy, asthma, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis, in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the light chain variable region of murine monoclonal antibody 2C4. This antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for detecting the presence of a cell, especially ecsinophil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antipooliferative drugs or radiomuclides to kill cells in areas of excessive SAF-2 expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG63991-93 represent the complementarity determining regions (CDRs)
allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
leukemia; eosinophil.
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Pred. No. 7.8e+05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bochner B, Erickson-Miller CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (UYJO ) UNIV JOHNS HOPKINS.
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66.7%;
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                                                                                                                                                                                                                                                                                                                                       07-MAR-2000; 2000US-0187595.
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                                                                                           Mus sp.
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The invention describes an antigen-binding protein (1) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (1g) (1ght chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting anglogenesis; creducing endothelial cell proliferation; inhibiting anglogenesis; creducing endothelial cell proliferation; inhibiting wEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; cand in vivo and in vitro for investigative, diagnostic or treatment cubstantially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins production on the cantibody and which provide other antibody functions can be present. There the FC region (e.g., CH2 and CH3 for an IGG molecule) of a natural complementarity determining region L3 (CDRL3) incorporated into an extraction described in the method of the invention.
                                                                                                                                                    New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin light chain; hypervariable region; PAF; CDR; antibody; platelet activating factor receptor; murine; chimeric; anti-PAF; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 7.8e+05;
0; Mismatches 3; Indels
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66.7%; Pred
0; F
                                                                                                                                                                                                                             Claim 55; Page 57; 64pp; English.
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Best Local Similarity 66,7-
                                                                                                     WPI; 2002-106189/14.
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                                                                                                                    N-PSDB; AAS20282
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                                                                                                                                                                                                         This sequence represents the complementarity determining region (CDR) 3 of the light chain hypervariable region of an antibody recognising the platelet activating factor (PAF) receptor. The variable region of mouse anti-PAF receptor monoclonal antibody is useful for the preparation of chimeric antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                             Polypeptide comprising variable region of antibody recognising PAF receptor - useful for the preparation of chimeric antibody
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 30; DB 19;
66.7%; Pred. No. 7.8e+05;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain CDR3 of catalytic antibody 6A12.
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                                                                                                                                                                Claim 2; Page 10; 14pp; Japanese,
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(SUME ) SUMITOMO ELECTRIC IND CO
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                                                                                                                                                                                                                                                                                                                                                                       Cuery Match
Best Local Similarity 66.79,
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                                                  WPI; 1998-355043/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overdose; addiction.
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                                                                                                                                                                                                                                                                                                                                                      9 AA;
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subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treatment of the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment,
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                       DB 19; ... 7.8e+05; 3; Indels
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llarity 55.6%; Pred. No. 7.8e+05;
Conservative 1; Mismatches 3;
                                                                                                                                                                ; Score 30; DB 1
; Pred. No. 7.8e+
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain CDR3 of catalytic antibody 12H1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW39826 standard; peptide; 9 AA;
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                                                                                                                                                                   62.5%;
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                                                                                                                                                                                          Local Similarity 55.6
les 5, Conservative
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A novel composition has been developed which comprises an immunoglobulin (Ig) having an affinity constant (Ka) of at least 2 multiply (100000000 M-1 for binding to a predetermined human antigen. The present sequence represents a human light chain CDR3 region peptide which forms part of an immunoglobulin comprising a VkL15 segment, a Jk2 segment, and the present light chain CDR3 region. The articD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These autoinmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals of multiple isotypes by undergoing isotype switching. These animals contraction and can switch to encode apply roduce one or more subsequent contraction and can switch to encode apply roduce one or more subsequent contractions.
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                                                                                                                                                                     Ig; affinity constant; human; antigen, hybridoma; B cell; transgene; transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel anti-CD4 antibody produced by transgenic mice - used in the treatment of auto-immune disease etc.
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                                                                                                                                      Human immunoglobulin light chain CDR3 region peptide.
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                                AAW24776 standard; peptide; 9 AA.
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                                                                                                    03-DEC-1997 (first entry)
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Matches 5; Conservative
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RESULT 15
                AAW2477
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Db 1 QQYDSYPYT 9 Search completed: April 22, 2003, 13:30:30 Job time: 74 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBGOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBGOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBGOMB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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48
1 QQLVEYPFT 9
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                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Sequence 6, Appli	Sequence 61, Appl	Seguence 47, Appl	Sequence 48, Appl		Sequence 23, Appl		Sequence 12, Appl	Sequence 28, Appl	Sequence 20, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 50, Appl	Sequence 61, Appl	Sequence 6, Appli	Sequence 4, Appli		Sequence 61, Appl	Sequence 19, Appl	Sequence 13, Appl	Seguence 6, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 32, Appl	Sequence 88, Appl	Sequence 26, Appl	
9 9 US-09-996-288-6	9 9 US-09-996-288-61	9 9 US-10-144-644-47	9 9 US-10-144-644-48	9 10 US-09-796-848A-7	9 10 US-09-796-848A-23	9 9 US-09-782-672-53	9 9 US-10-144-644-12	9 10 US-09-910-059-28	9 9 US-10-161-145-20	9 10 US-09-808-037-18	9 10 US-09-809-739-4	9 10 US-09-974-449-50	9 9 US-09-423-800-61	9 9 US-09-875-221A-6	9 9 US-10-015-535-4	9 9 US-09-269-921-5	9 9 US-10-182-018-61	9 10 US-09-286-240-19	9 10 US-09-954-166-13	_	9 10 US-09-434-965-1	7 10 US-09-870-472-13	8 9 US-10-046-801-32	9 9 US-09-900-290-88	9 9 US-09-782-672-26	
20 25 52.1	21 25 52.1	22 25 52.1	23 25 52.1	24 25 52.1	25 25 52.1	26 24 50.0	27 24 50.0	28 24 50.0	29 23 47.9	30 23	31 23 47.9	32 23 47.9	33 22 45.8	34 22 45.8	35 22 45.8	36 22 45.8	4	38 22 45.8	22 4	4	41 22 45.8	4	43 21 43.8	44 21 43.8	45 21 43.8	

## ALIGNMENTS

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US-09-976-787-6

USESULT INCOMMATION

SEQUENCE 6, Application US/09976787

SEQUENCE 6, Application US/09976787

SEQUENCE 6, Application US/09976787

SEQUENCE 7. Zenoping

NELLANT: ZUL Zenoping

PRIOR PLILING DATE: 11245/46505

CURRENT FILING DATE: 2000-10-28

PRIOR PLILING DATE: 2000-10-28

PRIOR PLILING DATE: 1099-01-29

PRIOR PLILING DATE: 1999-01-29

PRIOR PLILING DATE: 1999-01-29

NUMBER 0F SEQ ID NOS: 40 for Windows

SEG ID NOS FOR SEG ID WIND
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US=10-091-313-6
Sequence 6, Application US/10091313
Sequence 6, Application No. US2003004406A1
Sequence 6, Application No. US2003004406A1
GENERAL INFORMATION:
APPLICANT: DINGIVAN. CHRISTIN E
TITLE OF INVENTION: BROPHYLACTIC OR THERATING INFLAMMATORY OR AUTOIMMUNE
TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS
TITLE OF INVENTION: DISORDERS BY ADMINISTERING CD2 ANTACONISTS IN COMBINATION WITH O
TITLE OF INVENTION: DISORDERS: US/10/091,313
CURRENT APPLICATION NUMBER: US 60/273,098
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-10-19
SPRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 13
SOFFWARE: PATENTIN VEFSION 3.1
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                        56.2%; Score 27; DB 9; Length 9; llarity 50.0%; Pred. No. 2.7e+05; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-10-032-482-14
                            Query Match
Best Local Similarity
Matches 4; Conserv
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Patent No. US20020168360A1

GENERAL INPORMATION:

APPLICANT: DINGIVAN, CHRISTINE A.

TITLE OF INVENTION:

COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US 10/091,236

CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR PILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-11

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 16

LENGTH: 9

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Butcon, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
TITLE OF INVENTION: 20100mmune disease
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
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                                                                                                                                                                                                                                    Score 31; DB 10; Length 9; Pred. No. 2.7e+05; 0; Mismatches 3; Indels
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-6
                                                                                                                                                                                                                                      64.6%;
                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-09-828-708-51
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; ORGANISM: Mus sp.
US-10-091-236-16
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US-10-091-236-16
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US-09-828-708-51
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Jiao, Jin-an
Esperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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STREET: 130 Water Street
CITY: Boston
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54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.7e+05;
Matches 5; Conservative 1; Mismatches 3; Indels
                                      Score 27; DB 9; Length 9; Pred. No. 2.7e+05; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/814,806
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COLLEGE, PECEL F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ONIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-293-854-7
                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09293854; Patent No. US20020168357A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
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                                      h 56.2%;
Similarity 50.0%;
4; Conservative 1
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
                                      Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-996-288-16
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US-09-293-854-7
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Publication No. US20030068320A1

GENERAL INFORMATION:
APPLICANT: DINGIVAN, CHRISTINE A

TITLE OF INVENTION: METHODS OF ADMINISTERING/DOSING CD2 ANTAGONISTS FOR THE PREVENTIC

TITLE OF INVENTION: AND TREATMENT OF AUTOIMMUNE DISORDERS OR INFLAMMATORY DISORDERS
FILE REFREENCE: 10271-054-999

CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR APPLICATION NUMBER: US 60/273,098

PRIOR APPLICATION NUMBER: US 60/273,098

PRIOR FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS
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                                56.2%; Score 27; DB 9; Length 9; 50.0%; Pred. No. 2.7e+05; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09155106

Publication No. US20030054003A1

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINC
TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY
TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
NUMBER OF SEQUENCES: 45
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
PRICE OF THE STATEM TO STATEM TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Matches 4; Conservative
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
Query Match
Best Local Similarity
-Loc 4; Conserve
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                                                                                                                                                       2 QLVEYPFT 9
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5 EYPYT 9
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US-10-091-268-6
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Sequence 17, Application US/09808037

Sequence 17, Application US/09808037

Fatent No. US2002052311A1

GENERAL INFORMATION:

APPLICANT: SCLOWON, Beka

APPLICANT: SCLOWON, BERA

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: NEUTHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NEUTHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NEUTHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NUMBER: US/09/808,037

CURRENT APPLICATION NUMBER: US 09/473,653

PRIOR PILING DATE: 1999-12-29

PRIOR PILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Version 3.0

SEQ ID NO 17
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Patent No. US2002052311A1

GENERAL INFORMATION:

APPLICANT: SOLOWON, Beka

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

CURRENT APPLICATION NUMBER: US/09/808,037

CURRENT PILING DATE: 2001-03-15

PRIOR PELLING DATE: 2000-07-31

PRIOR FILING DATE: 2000-07-31

PRIOR PELLING DATE: 2000-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 9; Length 9;
Pred. No. 2.7e+05;
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Pred. No. 2.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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             PRIOR APPLICATION NUMBER: 09/129,026
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 08/905,825
PRIOR FILING DATE: 1997-08-04
NUMBER: OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                  54.2%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-808-037-19
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Sequence 16, Application US/0996288

Patent No. US20020177126A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Lealie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTMARE: Patentin version 3.1
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US-09-977-797A-62
i Gequence 62, Application US/09977797A
i Publication No. US20030044772A1
i General INFORMATION:
i GENERAL INFORMATION:
i APPLICANT: Watkins, Jeffrey D.
i APPLICANT: Wu, Herren
i TILE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
i TILE PREFERENCE: AME-06805
i CURRENT APPLICATION NUMBER: US/09/977,797A
i CURRENT APPLICATION NUMBER: 08/129,026
i PRIOR PRILING DATE: 1998-08-04
i PRIOR FILING DATE: 1998-08-04
i PRIOR FILING DATE: 1997-08-04
i NUMBER OF SEQ ID NOS: 136
i SEQ ID NO 62
i LENGTH: 9
i LENGTH: 9
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US-09-977-797A-66
Sequence 66, Application US/09977797A
Sequence 66, Application US/09977797A
Sequence 66, Application No. US20030044772A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Waskins, Veifrey D.
APPLICANT: Wu, Herren
TITLE REPERENCE: AME-06805
FILE REPERENCE: AME-06805
CURRENT APPLICATION NUMBER: US/09/977,797A
CURRENT FILING DATE: 2002-06-25
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Pred. No. 2.78+05;
Transcription of the control of the 
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62.5%;
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Best Local Similarity 62.5
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Best Local Similarity 55.0.
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US-09-996-288-16
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; ORGANISM: Homo sapiens
US-09-977-797A-62
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## Sequence 2, Application US/09994078

## Publication No. US20030032774A1

## SPELICANT: BROWN, WILLIAM

## APPLICANT: BROWN, WILLIAM

## APPLICANT: MARTEL, RENE

## APPLICANT: MARTEL, RENE

## APPLICANT: MARTEL, RENE

## APPLICANT: MARTEL, PIERRE

## APPLICANT: MARTEL, PIERRE

## APPLICANT: MARTEL, PIERRE

## APPLICANT: MARTEL, PIERRE

## APPLICANT: WARTEL, PIERRE

## APPLICANT: WAS 1923/28237

## CURRENT APPLICATION NUMBER: 08/199,518

## PRIOR FILING DATE: 1998-03-03

## PRIOR PILING DATE: 1996-10-02

## PRIOR PILING DATE: 1996-10-02

## SEQ ID NO 2

## ELENGTH ## APPLICATION NUMBER: 08/718,585

## PRIOR PILING DATE: 1996-10-02

## SEQ ID NO 2

## ELENGTH: ##

## TUBLE OF SEQ ID NOS: 3

## SOFTWARE: PATENT!

## TUBLE OF SEQ ID NOS: 3

## TUBLE OF SEQ ID NOS: 3
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JOTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-994-078-2
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PRIOR FILING DATE: 1999-12-29
PRIOR PELICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SEO TWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic peptide US-09-808-037-19
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-994-078-2
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Search completed: April 22, 2003, 13:39:11 Job time : 42 secs

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Query Match
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RESULT
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Sequence 1,
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Sequence 2
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           GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-214-095D-27

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US-09-214-095D-21

US-09-406-532-20

US-08-48-133-3

US-08-464-093-26

US-08-672-345C-34

US-08-672-345C-30

US-08-114-095D-30

US-09-214-095D-30

US-08-114-095D-30

US-08-14-095D-30

US-08-14-095D-30

US-08-974-899-15

US-08-974-899-15

US-08-974-899-15

US-08-974-899-15

US-08-974-899-15

US-08-974-899-15

US-08-974-899-15

US-08-444-818-362

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-170-769A-24

US-09-170-769A-24

US-08-171-77
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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48
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
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ZIP: 10036

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Ploppy disk COMPUTER: Parentin Release #1.0, Version #1.30 SOCTWARE: Parentin Release #1.0, Version #1.30 APPLICATION NUMBER: US/08/672,345C FLING DATE: 24-UN-1996

CURRENT APPLICATION: 435

ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: 212-391-0525

TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION
GENERAL INVENTION
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
       US-08-627-173-6

US-08-535-882A-6

US-08-505-546-6

US-08-507-173-5

US-08-131-882A-5

US-08-131-882A-5

US-08-131-88-24

US-08-150-260A-524

US-08-150-260A-524

US-08-150-260A-64

US-08-470-110A-48

US-08-470-110A-48

US-08-470-110A-48

US-08-677-769A-47

US-08-677-769A-47

US-08-677-769A-48

US-08-677-769A-47

US-08-677-769A-48

US-08-677-769A-47

US-08-677-769A-48
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Local Similarity 88.9%;
nes 8; Conservative
STRANDEDNESS: single
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Gaps
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Pred. No. 1.9e+05;
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US-08-438-123-3
Sequence 3, Application US/08438123
Patent No. 5552293
GENERAL INFORMATION:
APPLICANT: Lindholm et al
TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
TUTBE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                 GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FIRE REPERSIVE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-406-532-20

US-09-406-532-20

Sequence 20, Application US/09406532A

Patent No. 6365154

GENERAL INFORMATION:

APPLICANT: Connie L. Erickson-Miller

APPLICANT: James D. Winkler

TITE OF INVENTION: TIEZ Agonist Antibodies

FILE REFERENCE: P50843

CURRENT APPLICATION NUMBER: US/09/406,532A

CURRENT APPLICATION NUMBER: 06/102,098

PRIOR APPLICATION NUMBER: 60/102,098

PRIOR APPLICATION NUMBER: 60/102,098

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 20

LENGTH: 9

TURNED: NOW: 10
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v 66.7%; Pred. No. 1:-
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; OTHER INFORMATION: light chain CDR 3
US-09-406-532-20
                                 RESULT 4
US-09-214-095D-21
Sequence 21, Application US/09214095D
; Patent No. 6280987
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7.
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Murinae gen.sp.
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 6; Conserva
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1 QHFVDYPFT 9
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LENGTH: 9
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
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US-08-672-345C-21
Sequence 21, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
           Sequence 27, Application US/09214095D
Patent No. 6200987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT PILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                      91.7%;
88.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Matches 6; Conservative
                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Murinae gen. sp.
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Best Local Similarity 88.9
Matches 8; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
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US-09-214-095D-27
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Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 32; DB 1; Length 9; 62.5%; Pred. No. 1.9e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elap PC Compatible
COMPUTER: Elam PC Compatible
OPERATION SYSTEM: PC-05/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INNERAMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28 678
REFERENCY/POCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
         NOVOP/106A/7551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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US-08-672-345C-30
; Sequence 30, Application US/08672345C
                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
REFERENCE/DOCKET NUMBER: NOV TELECOMMUNICATION: TELEPHONE: (416) 868-1482 TELEPHONE: (416) 362-0823 INPORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
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55.6%;
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Best Local Similarity 55.0
---- 5, Conservative
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 62.5
Matches 5; Conservative
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STRANDEDNESS: single
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US-08-672-345C-24
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APPLICANT: Michael D. Dan
TITLE OF INVENTION: HURAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: HURAN MATIGEN
TITLE OF INVENTION: ANTIGEN
TOWNERS:
ADDRESSE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STREET: Onterio
CUNTRY: Canada
ZIP: M5H 2J7
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:

**APPLICATION NUMBER: US/08/264,093
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Pred. No. 1.9e+05;
1; Mismatches 1; Indels
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PRIOR APPLICATION DATA: No. 5639863 applicable ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
      T: Suite 300, 99 Canal Center Plaza
'ADDRESSEE: Lowe, Price, LeBlanc & Becker
                                                                                                                        COUNTAIL COLUMINITY COUNTAIL COUNTAIL COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: J.G. Mullins
REGISTRATION NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFO
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Patent No. 5639863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                   STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QHLEYPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-264-093-26
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62.5%; Score 30; DB 4; Length 9; 55.6%; Pred. No. 1.9e+05; ive 1; Mismatches 3; Indels
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Pred. No. 1.9e+05;
                      RESULT 11
US-09-214-095D-30
Sequence 30, Application US/09214095D
Sequence 30, Application US/09214095D
Sequence 30, Application US/09214095D
GENERAL INFORMATION:
APPLICANT: Landary, Donald
TITLE OF INFORMATION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ALLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Section (1) Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
ITLE OF INVENTION: HUMANIZED ANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGIGSTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-30
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Best Local Similarity
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US-08-116-778E-11
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LENGTH: 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVEXTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-214-095D-24
; Sequence 24, Application US/09214095D
; Patent No. 6280967
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; FILLE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILLING DATE: 1999-07-19
; NUMBER OF SILLING SECOND NOS: 121
; SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPYTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:.

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPRICE JOGGET NUMBER: 0575/51400

TELEPRICE JOGGET JOG
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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LENGTH: 9
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Fatent No. 6037454
GENERAL INFORMATION:
- APPLICANT: Presta, Leonard G.
- APPLICANT: Presta, Leonard G.
- TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCES. 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
- STREE: California
- COUNTY: South San Francisco
- STATE: California
- COUNTY: USA
                              APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SECONDRESS:
ADDRESSE: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
CONTRY: U.S.A.
ZIP: Z2201-4714
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION NUMBER: US/08/483,528B
FILING DATE: (703)816-4000
THEREPAK: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMFUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: WIDBALIN (Genentech)
CURENT APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
NTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 91014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0
Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-483-528B-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QQLVEYPFT 9
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             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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          3; Indels
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Pred. No. 1.9e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,562

CLASSIFICATION DATA:

FILING DATE: UO-MAY-95

CLASSIFICATION NUMBER: 08/116,778

FILING DATE: 0-SEP-93

CLASSIFICATION NUMBER: 08/116,778

FILING DATE: 0-SEP-93

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 249-76

TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHIZARA, KENYA
APPLICANT: HANII, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: ADRESS:
CORRESPONDENCE ADDRESS:
      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-483-528B-99
Sequence 99, Application US/08483528B
Sequence 99, Application US/08483528B
SEGUENCE OF 59362B-5
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: STOTKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
CITY: ARLINGTON
STATE: URGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08438562
Patent No. 5874255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)816-4100
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.3%;
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Best Local Similarity 55.6
Matches 5; Conservative
   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-438-562-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
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                                                                  1 QQLVEYPFT 9
                                                                                                                           1 QORSSYPYT 9
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                                                                                                                                                                                                                        RESULT 13
US-08-438-562-11
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Matches
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                                                                                                                                                                                                                                                                                                        Search completed: April 22, 2003, 13:32:17
Job time : 15 secs
TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
ILENGTH: 9 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
US-08-974-899-15
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April 22, 2003, 13:38:27 ; Search time 43 Seconds (without alignments) 11.178 Million cell updates/sec
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                       Run on:
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US-09-674-716B-9 33

1 GYWMS 5 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

206 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 5 Minimum DB Maximum DB

summaries 100% Post-processing: Minimum Match 00* Maximum Match 100* Listing first 45

PIR Database

1: pirl: * 2: pirl: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COI intron 16 prot 1g heavy chain CRD surface protein te R-phycoerythrin al TRH-like tripeptid globulin IV alpha Ig heavy chain CRD bradyklnin-potenti RPCH-related neuro T-cell receptor be T-cell receptor be neuropeptide - sea bradykinin-potenti Ig heavy chain CRD gene p20K protein acharin-1 - giant URF2 protein - Xan pap fimbrial regul dnaZX-like protein hypoxanthine phosp Leu-enkephalin - b Met-enkephalin - b I-cell receptor be I-cell receptor be carbon-monoxide de cocoonase (EC 3.4. growth-modulating gut pentapeptide cholecystokinin-5 Description SUMMARIES A32516 S09478 PT0308 F37196 A34626 B53284 PT0661 A60803 A70281 PT0729 PT0729 150412 A32480 S70154 B37325 I40469 BB Query Match Length Score Result

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Gaps

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0; Indels Length 5;

Query Match
48.5%; Score 16; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;

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blood cell protein	tyrogine-melanocyt	phenol 2-monooxyge	protamine P1 - ora	Ig heavy chain CRD	Ig mu chain V regi	protamine P1 - Cer	protamine P1 - sav	Ame	ribosomal protein	ribosomal protein	ribosomal protein	major protein anti	R-phycoerythrin ga	angiotensin-conver	photosystem I 10.4	
3 S68328	2 A32039	2 A37832	2 I61883	2 PT0240	2 S43959	2 137013	2 I84439	1 HOROHA	2 I39964	2 I39966	2 I39965	2 E60274	2 F22565	2 PQ0009	2 PQ0689	
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7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	7 21.2	
30	31	32	33	34	35	36	37	• 38	39	40	41	42	43	44	45	

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A33216
cholecystokinin-5 - dog
NiAlternate names: CCK-5
Clobecies: Canis lupus familiaris (dog)
Cj.Species: Taleoct-1989 #sequence_revision 18-oct-1989 #text_change 18-Aug-2000
Cj.Species: Taleoct-1989 #sequence_revision 18-oct-1989 #text_change 18-Aug-2000
Cj.Species: Taleoct-1892, J.; Reeve Jr., J.R.; Bysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A.Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest
A.Reference number: A32516
A.Reference number: A32516
A.Residues: J-5 calls
Cj.Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystoking comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystoking Cj.Superfamily: gastrin
Cj.Superfamily: gastrin
Cj.Superfamily: amidated carboxyl end, neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental
THOSES Anguilla japanese eel (2.5pecies: Anguilla japanese eel (2.5pecies: Anguilla japanese eel (2.5pecies: Anguilla japanese eel (2.5pecies: Anguilla japanica (Japanese eel) (2.5pecies: Japanese eel) (3.5pecies: Japanese eel) (3.5pecies: Japanese: Anguilla (Japanese: Japanese: J
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Best Local Similarity 66.7%;
Matches 2; Conservative 1
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1 GFW 3
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RPCH-related neuropeptide - ferruginous spindle
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Species: Pusinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762; PMID:2310394
A;Accession: A34626
A;Accession: A34626
A;Accession: A34626
C;Keywords: neuropeptide
C;Keywords: neuropeptide
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C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: O2-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C.Accession: B53284
R.Harindranath, N.; Alexander, C.B.; Mage, R.G.
A.O. Immunol. 28, 881-888, 1991
A.Title: Evolutionarily conserved organization and sequences of germline diversity and j
A.Reference number: A53284; MUID:91342695; PMID:1678859
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C;Specias: Mas musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0661
R;Feeney, A.J.
C;Accession: PT0661
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0609; MUID:91277601; PMID:1711558
A;Reference number: PT0609; MUID:91277601; PMID:1711558
A;Reference number: A;Reference number: PT0661
A;Reference number: PT0
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A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0;
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33.3%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-4 < HAR.>
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                                                                                                                                                 Globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
NyAlternate names: 11S globulin alpha subunit gamma chain
NyAlternate names: 11S globulin alpha subunit gamma chain
Syspecies: Cucurbita sp. (cucurbit)
Cjbate: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
CjAccession: S09478
Nobmiyar, M.; Hara, I.; Matushara, H.
Plant Cell Physiol. 21, 157-167, 1980
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A;Reference number: S0966
A;McCession: S09478
A;McCession: S09478
A;McCession: L-4 <0HM>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Accession: P70308
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J; Exp. Med. 173, 395-407, 1991
A; Tile: Preferential utilization of specific immunoglobulin heavy chain diversity in A; Reference number: P7022; MuID: 9110837; PMID: 1899102
A; Reference number: P7022; MuID: 91108337; PMID: 1899102
A; Residues: 1-5 < VAM>
A; Residues: 1-5 < VAM>
A; Residues: 1-5 < VAM>
A; Residues: Homo source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.4%; Score 13; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 2; Conservative
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Gaps

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Length 5;

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T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PT0640; PT0685; PT0729
B;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Retersion: PT0640
A;Status: translation not shown
A;Status: translation not shown
A;Residues: 1-5 <FES>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Residues: 1-5 <FES>
A;Residues: 1-5 <FES
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C;Species: Mus musculus (house mouse)
C;Daccies: Mus musculus (house mouse)
C;Accession: P10580
B;Feeney, A.J.
C;Accession: P10580
B;Feeney, A.J.
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: P10580
A;Reference number: P10580
A;Reteresion: P10580
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A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0;
                                                         A, Experimental source: B lymphocyte
C, Keywords: heterotetramer; immunoglobulin
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bradykinin-potentiating peptide 7 - island jararaca
C,Species: Bothrops insularis (island jararaca)
C,Date: 14-Peb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C,Accession: G37196
R,Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A,Title: Primary structure and biological activity of bradykinin potentiating peptides
A,Reference number: A37196; MUID:90351557; PMID:2386615
A,Ression: G37196
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-5 <CIN>
C,Reywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C;Speciae: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M; Masserman, R; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Molecule type: DNA
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33.3%; Score 11; DB 2; Length 4;
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c;Species: Gallus gallus (chicken)
c;Species: Gallus gallus (chicken)
c;Species: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Ccession: 150412
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
d; Biol. Chem. 268, 8131-8139, 1993
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken A;Reference number: A46643; MUID:93216790; PMID:8463325
A;Accession: 150412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3 <MAO>
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tive 0; Mismatches 0; Indels
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A.Contents: annotation; X-ray crystallography, 0.85 angstroms
A.Note: achatin-II has L-phenylalanine
C.Keywords: D-amino acid
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                                                      April 22, 2003, 13:32:21 ; Search time 11 Seconds (without alignments) 18.853 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                      - protein search, using sw model
                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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RE32
ACH1
OCP1
OCMM
DCMM
FAR3
FAR4
FYRI
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UXA4
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PSK D
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BIOA
BIOA
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                                                                                         US-09-674-716B-9
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1 GYWMS 5
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Match
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                                      OM protein
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                                                         Run on:
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                        sus scrofa
vibrio fisc
homo sapien
escherichia
acheta dome
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Iwakoshi B., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
Peptides 21:623-630(2000).
-!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less
active than Ocp-3.
-!- SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
01-FEB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutenta; Rodentia; Sciurognathi; Muridae; Musinae; Musl.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Octopus minor (Octopus).

Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
Incirrata; Octopodidae; Octopus.

NCBI_TAXID=89766;
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                        P01151
P24272
P01858
P13973
  P19991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 1; Length 4; Pred. No. 1.1e+05; 0; Migmatches 1; Indels
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4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
-1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Cardioactive peptides Ocp-3/Ocp-4.
                                                                                                                                                                                                                                                                                                            4 AA.
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  SUGA_ACHDO
THYL_PIG
LUXE_VIBFI
TUFT_HUMAN
TRM3_ECOLI
                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
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MOD RES 2 2
SEQUENCE 4 AA; 463 N
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UF01 MOUSE
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TISSUE=Fibroblast,
MEDLINE=95009907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 19 kDa.

5 AA; 717 MW; 7364087043100000 CRC64;

NON TER SEQUENCE

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RESULT 5
RE32_LITRU
ID _RE32_LITRU
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P35904;
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1 GFF 3
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SEQUENCE
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sea moses sole (Pardachirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINES-9031557; PubMed=2386615;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227 (1990)
J. Protein Chem. 9:221-227 (1990)
I. Protein Chem. 9:221-227 (1990)
I. FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ARGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.

PIR; G37196; G37196.
                                                             Gaps
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30-MX-2000 (Rel. 39, Last sequence update)
16-OCT-2000 (Rel. 40, Last annotation update)
16-OCT-2000 (Rel. 40, Last annotation update)
Pardachi II (PXII) (Fragment).
Pardachirus marmoratus (Red sea moses sole).
Pardachirus marmoratus (Red sea moses sole).
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Nooteleostei, Acanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes;
Soleidei, Soleidae, Pardachirus.
                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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                   Score 15; DB 1; Length 5; Pred. No. 1.18+05; 0; Mismatches 1; Indels
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Pred. No. 1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ļ
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                     45.5%;
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                                                             Conservative
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                   Query Match
Best Local Similarity
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P81864;
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P30425;
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BOTIN
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Achatinacea, Achatinidae, Achatina.
NCBI_TaxID=6530;
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                                                                                                                                                                                                                                                                                                                                                            Gaps
-i- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURPACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
-i- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Lilori electrica. Comparison with the skin peptides from Litoria rubella.", Chem. 52:639-645(1999).
-I- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
STRAIN=Ferusac; TISSUE=Ganglion;
MEDLINE=89273551; PubMed=2597281;
Kamateni Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
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                                                                                                                                                                                                                5 AA; 614 MW; 7769C9C9C8100000 CRC64;
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llarity 33.3%; Pred. No. 1.1e+05;
Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                               30.3%; Score 10; DB 1; I
33.3%; Pred. No. 1.1e+05;
iive 2; Mismatches 0;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Litoria rubella (Desert tree frog).
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                                                                                                                                                                                                                                                                                                                       Growth-modulating peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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21-JUL-1986
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P01157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (H-G1y-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid residue.";

Int. J. Pept. Protein Res. 39:258-264(1992)

AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY NEURON (FON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.

PIR; A32480; A32480.
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Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
                                                                                                                                              STRAIN=Ferussac; TISSUE=Heart atrium; MBDLINE=91264856; PubMed=1675568; PubMed=1675568; Pujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
Fulica Ferusaac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93014529; PubMed-1399265;
Ishida T., In Y., Dol M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
Ilwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoundation update)
15-JUN-2002 (Rel. 41, Last amoundation update)
Cardioactive peptides Ocp-1/Ocp-2.
Octopus minor (Octopus).
Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Octopoda, Incirrata, Octopodidae, Octopus.
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Peptides 21:623-630(2000).
-!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
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Pred. No. 1.1e+05;
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4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AA; 408 MW; 6AADD9C81000000 CRC64;
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-!- MASS SPECTROMETRY: WW=395.2; METHOD=MALDI.
Hormone; D-amino acid.
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Matches 1; Conserv
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Best Local Similarity
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acceptor.
-!- COFACTOR: Molybdenum (molybdopterin).
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
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"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
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                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=77162369; PubMed=858356; Schlesinger D.H., Pickart L., Thaler M.M.; Schlesinger D.H., Pickart L., Thaler M.M.; Experientia as:1314-325(1977) Experientia as:1324-325(1977) Experientia as:1324-325(1977) -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULA GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas carboxydohydrogena.
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Bradyrhizobium group.
NCBI_TaxID=290;
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JW1-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (BC 1.2.99.2)
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Pred. No. 1.1e+05;
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                                                         21-UU-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
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Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of RPamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.

**BEDINES-2195954; PubMed=1686933;

**Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

**Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

**Identification of RFamide neuropeptides in the medicinal leech.";

**Peptides 12:897-908(1991).

-!- SIMILARITY: BELONGS TO THE PARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YLRF-amide.
Hirudo medicinalis (Medicinal leech)
ENkaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellia; Hirudiniformes; Hirudinidae; Hirudinea;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
FMRFamide-like neuropeptide YMRF-amide.
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
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4 AA; 598 MW; 69D4073B3000000 CRC64;
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100.0%; Pred. No.
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Conservative
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Crustacea;
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McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188 (1993)
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Atcho-Rlamide I (Contains: Antho-Rlamide II].
Authopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nymantheae; Actiniidae; Anthopleura.
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Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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                                                                                                                                                                                                                                                                                                            Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P.;
Grimmelikhuijzen C.J.P.;
"Isolation of two novel neuropeptides from sea anemones: the biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its Ges-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60441B59A0000000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTHO-RIAMIDE I.
ANTHO-RIAMIDE II.
L-3-PHENYLLACTYL.
AMIDATION.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
  4 AA.
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-- SUBCELLULAR LOCATION: Secreted.
-- TISSUB SPECIFICITY: Neuron-specific.
InterPro: IPR001023; HSp70.
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STANDARD;
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Terricola; Geoplanidae; Arthurdendyus.
NCBI_TaxID=132421;
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MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Matazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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SEQUENCE, AND SYNTHESIS.
MEDLINE=94211927; PubMed=7909164; // Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L., Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L., RYIRPamide: a turbellarian FMRFamide-related peptide (FaRP)."; Regul. Pept. 50:37-43(1994).
-! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                          21.2%; Score 7; DB 1; Length 5; ilarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indele
          Neuropeptide; Amidation; Multigene family.
MOD RES 5 AMIDATION (POTENTIAL).
SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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SEQÜENCE 5 AA, 754 MW; 69D4004B44600000 CRC64;
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(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PWRFamide-like neuropeptide RYIRF-amide.
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Life Sci. 17:1253-1256(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation.
MOD_RES 5 5
                                                                                                                                                                                             STANDARD;
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SPECIES=P.americana;
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Best Local Similarity
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01-FEB-1995 (
Proctolin.
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MEDLINE=66232789; PubMed=2872661;
Stangier J., Dircken H., Keller R.;
Stangier J., Dircken H., Keller R.;
Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
-1- FUNCTION: STIMILATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
PIR; A01644; HOROHA.
PIR; A60411; A60411.
                                                                                                                                                                                                                                                                                                                       "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
MEDLINE-81225865; PubMed-6113690; O'Shea M., Adams M.E.; "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                   SPECIES=L.polyphemus;
MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 7; DB 1; Length 5; 100.0%; Pred. No. 1.1e+05; ive 0; Mismatches 0; Indels
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Best Local Similarity
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SEQUENCE 5 A
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Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
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Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination; Calcium; Multigene family.
NON TER
                                                                                                                                       STRAIN=HIMMLAYA; TISSUE=ALEURONE LAYER; MEDLINE=91329704; PubMed=1831055; Jacobsen Jv., Close T.J.; Close T.J.; Close T.J.; Close T.J.; aciden the expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley
                                                                                                                                                                                                                      aleurone layers.";
Plant Mol. Biol. 16:713-721(1991)
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-!- MISCELLANBOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
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NCBI_TaxID=1396;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10-OCT-2001 (TrEMBLrel. 18, Last annotation update)
88 kDa protein (Fragment).
Bacillus cereus.
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Submitted (JUL_2001) to the SWISS-PROT data bank.
NON TER 5 5
SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64
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01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotati
PMRFamide-like neuropeptide (LPLRFamide)
Alpha-amylase (EC 3.2.1.1) (Fragment)
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STRAIN=NCIMB 11796;
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SEQUENCE FROM N.A.
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                                                                                                    April 22, 2003, 13:37:57 ; Search time 82 Seconds (without alignments) 12.564 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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sp_rodent:*
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Match Length DB
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01-NOV-1996
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                               TISSUB-BRAIN;
PubMed=6137771;
PubMed=6137771;
PubMed=6137771;
"A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";
Nature 305:328-330(1983).
-I- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELAIED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato H., Aono S., Kashiwamata S., Koiwai O.,
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.",
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
-!- FUNCTION: UDPGT IS OF MAJORE IMPORTANCE IN THE CONUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
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Transferase; Glycosyltransferase; Microsome; Multigene family.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
UDF-2Jucurconosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.1%; Score 3; DB 13; Length 5; Best Local Similarity 0.0%; Pred. No. 6.7e+05; Matches 0; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AA; 645 MW; 69D4073767400000 CRC64;
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-!- SUBCELLULAR LOCATION: MICROSOME.
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                                                                                                                                                                                           SEQUENCE, AND SYNTHESIS.
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                                                                                                                   NCBI_TaxID=9031;
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SEQUENCE 5
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April 22, 2003, 13:32:01 ; Search time 33 Seconds (without alignments) 20.189 Million cell updates/sec
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Run on:

24944 Total number of hits satisfying chosen parameters: 908470 segs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GYWMS 5 Title: Perfect score: Scoring table: Sequence: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

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3: SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ជា	AAY32257	AAR62882	AAR97316	AAY05038	AAB61293	AA017609	AAU75739	AAR76079	AAE22200	AAR85499
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## ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; Sjogren's syndrome; altergy, asthma; thintis; eczema; insulitis; graft.versus-host disease; COPD; bronchitis; diabetes; Light chain CDR H1 of mouse anti-CD23 MAb C11. AAY32257 standard; Peptide; 5 AA. B-cell malignancy; therapy. (first entry) 15-FEB-2000 AAY32257; RESULT 1 AAY32257 

99WO-GB01434. WO9958679-A1. Mus musculus 07-MAY-1999; 8-NOV-1999

98GB-0009839. (GLAX ) GLAXO GROUP LTD. 09-MAY-1998;

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New humanised anti-CEA monoclonal antibody - having engrafted murine CDRs, used for diagnosis, imaging and therapy of CEA-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanised monoclonal antibodies (MAbs) comprising the complementary determining regions (CDRs) of a parental murine class III anti-carcinoembryonic (CBA) MAb engrafted to the framework regions (FRs) of a heterologous antibody which can be derived from any species including human, retain the anti-CBA binding specificity
                                                                                                                                                                                                               Mice were immunised with an extract of human atherosclerotic plaque, then spleen cells were fused with SP2/01-Ag-14 myeloma cells. Hybridomas were screened by ELISA for reactivity with the immunogen and clone 22D3 was isolated. The Z2D3 antibody reacts specifically with atherosclerotic tissue; it recognises a non-protein antigen containing cholesterol (or similar steroid that is a substrate for cholesterol vaidase) and aquaternary ammonium salt (pref. a phosphalidylcholine or related compound that is a substrate for phosphalidylcholine or related compound that is a substrate for phosphalidylcholine or related compound that is a substrate for phosphalipase C). The CDR sequences for the heavy and light chains of Z2D3 were determined; peptides comprising the CDRs are claimed,
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                                      New antigen comprising hydroxy:steroid and quat. ammonium salt and related antibodies, useful e.g. for imaging, ablating or treating atherosclerotic plaque, and detecting plaque specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 15; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                      Claim 199; Page 147; 288pp; English.
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Best Local Similarity
N-PSDB; AAQ78734
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                                                                                                                                                                                                                                                             (CDR HI) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also ANY32263). The invention provides altered antibodies, wuch as chimeric or humanised antibodies, which comprise sufficient of the antho acid sequences of C11 light and heavy chain CDRs (see ANY3254-59) to render them capable of binding to the CD23 C type II molecule expressed on haemacopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowed lisease, allorgic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, colitis, Crohn's disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atherosclerosis, atherosclerotic plaque, anti-hydroxysteroid antibody, murine monoclonal antibody, heavy chain variable region: CDR1, complementarity determining region; imaging; plaque ablation.
                                                                                                                        Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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Shearin J;
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Rapson NT,
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Crowe SJ, Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR62882 standard; peptide; 5 AA.
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                                                                                                                                                                                             Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US04641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                              WPI; 2000-053101/04.
N-PSDB; AAZ34742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA;
Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calenoff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9425053-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Gaps

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This sequence represents a heavy chain complementarity determining region (CDR) from a tumour antigen specific antibody.

The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising: (a) selectively immobilising a diverse population of binding molecules to a solid support; (b) simultaneously contacting the diverse population immobilised on the solid support with 2 or more ligands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as targeting agents for cancer therapy that minimises impact on non-tumour
of the parental murine MAb but are less immunogenic in a human subject than the parental MAb. The humanised antibodies can be used in diagnosis, imaging and therapy of CEA-producing cancers and patients receiving the humanised antibodies and conjugates show decreased therapeutic results, decreased immune responses and decreased immune-mediated adverse effects compared to the parent entibody. This sequence is a murine derived CDR region which corresponds to CDR 1 in the heavy chain of the humanised MAb. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour antigen; antibody; CDR; complementarity determining region;
binding molecule identification; tumour-specific binding polypeptide;
cancer therapy; heavy chain.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two cmore ligands
                                                                                                                                                                                                   91.8%; Score 27; DB 17; Length 5; 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour antigen antibody heavy chain CDR1 clone F15.
                                                                                                                                                                                                                           100.0%; Pred. w...
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                                                                                                                                                                                                                                                                                                                                                                                                         AAY05038 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0905825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-153951/13.
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IXSY-) IXSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX28215.
                                                                                                                                                                               5 AA;
                                                                                                                                             AAR97313-97333.
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2 YWMS 5
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                                                                                                                                                                                                                                                                                     2 YWMS 5
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                                                                                                                                                                               Sequence
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The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein v (GPVI), also called TANGO 26s. The GPVI polymucleorides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombocic occlusion of the coronary artery diseases (e.g. stroke and isorders, coronary artery and cerebral artery diseases (e.g. stroke and isorders), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and cardiac isohaemia following angioplasty and metastatic cancers, especially of the colon and liver.
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                  Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiatreriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; ischaemia; cardiovascular disease; immunological disease; liver disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vainchencker W, Gill DS;
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and
                                                                                                ;
                                              Score 27; DB 20; Lengtn 5, Pred. No. 7,88+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Villelal J, Jandrot-Perrus M,
                                                                                                                                                                                                                                                                                                                                      Anti-TANGO 268 BCFv CDR, SEQ ID NO: 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 31; Page 102; 227pp; English.
                                                  81.8%; Scc_
100.0%; Pre/
0; }
                                                                                                                                                                                                                                      AAB61293 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1999; 99US-0345468.
06-DEC-1999; 99US-0454824.
14-FEB-2000; 2000US-0503387.
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                               Conservative
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                                                        Query Match
Best Local Similarity
                               5 AA;
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                              Sequence
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 tissues.
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Anti-(MCP)-1 antibody heavy chain protein hypervariable region CDR1.
                                                                                                                                              Human; antibody; MCP; monocyte chemoattractant; antiasthmatic; antiallergic; antinflammatory; idiopathic thrombocytopaenia; immunosuppressive; cytostatic; vasotropic; antiatratioslarctic; antirheumatic; antiarthritic; osteopathic; antigen-binding site; immunoglobulin heavy chain; monocyte migration; T cell migration; CC-type chemokine; eotaxin; allergy; allergic rhinitis; cancer; hypersensitivity response; allergic contact dermatitis; ancer; inflammatory bowel disease; althma; pooriasis; COPD; osteoporosis; inflammatory bowel disease; multiple sclerosis; autoimmune disease; rheumatoid archritis; diabetes; systemic lupus erythematosus; theumatoid archritis; diabetes; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                               bone disease; osteoporosis; osteoarthritis; periodontal disease; haematological disorder; haemolytic anaemia; graft rejection; leucocyte infiltration; restenosis; arteriosclerosis; CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
           AAU75739 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001; 2001WO-EP07468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000GB-0016138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiestand P, Hofstetter H,
                                                                              08-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                               AAU75739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stromal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, non-small-cell lung cancer, cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a peptide described in the exemplification of the
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                         Human, FAPalpha, fibroblast activating protein alpha, antibody, Ab, gene therapy, cancer, wound healing, inflammation, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mersmann M;
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                               Length 5;
                                                                                                                                                                                                                                                                                                                                         Human FAPalpha specific VL region from VH50 CDR1 peptide.
                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garin-Chesa P, Pfizenmaier K, Moosmayer D,
                               DB 22; L
                    81.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6C; 109pp; English.
                                                                                                                                                                                                                                 AAO17609 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-2000; 2000DE-1013286.
11-SEP-2000; 2000GB-0022216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001; 2001WO-EP04716
                                                                                                                                                                                                                                                                                                     08-AUG-2002 (first entry)
                                                                     Conservative
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Best Local Similarity
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N-PSDB; AAL46554.
                              Query Match
Best Local Similarity
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5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                     2 YWMS 5
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Schmidt A;
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                                                                                                                            2 YWMS
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                                                                                                                                                                                                                                                                 AA017609;
 Sequence
                                                                     Matches
                                                                                                                                                                                             RESULT 6
AAO17609
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Di Padova FE;

Urfer R,

Payne TG,

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This invention relates to a molecule that binds MCP-1 (human monocyte chemoattractant protein-1). The molecule has at least one antigen beinding site compilating at least one immunosjobulin (Ig) heavy and/or light chain variable domain (Wh. VI). The antibody of the invention inhibite binding of MCP-1 (and also eotaxin) to specific receptors, so preventing migration of monocytes and T cells. These are human creation with other human CC-type chemokines or MCP-1 from other antibodies with very high affinity for MCP-1, but no significant reaction with other human CC-type chemokines or MCP-1 from other species. The MCP-1 binding molecules, specifically antibodies that cross react with eotaxin, are used to prevent or treat MCP-1 or eotaxin-completed disorders, particularly those that involve migration or activation of monocytes and T cells, e.g. allergies (allergic rhinitis, thypersensitivity responses, allergic context dermatise), inflammatory bowel disease (athma, psoriasis, COPP, inflammatory bowel disease, contensity diseases (athma, psoriasis, COPP, inflammatory bowel disease, costeoarthritis, diopathic thrombocytopaenia) graft rejection, cancers that include leucocyte infiltraction, (rel stenosis, rejection, cancers that include leucocyte infiltraction, the present sequence represents the human anti-(MCP) arteriosclerosis, osteoarthritis, and many other diseases listed in the cancer in sequence hypervariable domain peptide CDRI of the
                                                                                                   New compound that binds human monocyte chemoattractant protein-1, useful e.g. for treating inflammation, comprises immunoglobulin chains with specific hypervariable regions
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 35; 42pp; English.
WPI; 2002-164525/21.
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DB 23; Length 5;

81.8%; Score 27;

Query Match

YWMS 5

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7 RESULT

Thu Apr 24

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy and light chains of MAb 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CAS5.1. It is optionally humanized and in the form F(ab/2, F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                      Antigen binding structure; complementarity determining region; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; Mab, immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
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                      Indels
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         7.8e+05;
hes 0;
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Pred. No. 7.8e+05;
1; Mismatches 0
         Pred. No. 7.8
Mismatches
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100.0%; Pre-
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                                                                                                                              AAR76079 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                    94WO-GB02610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.8%;
75.0%;
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93GB-0024819
                                                                                                                                                                                                 MAb 55.1 heavy chain CDR1.
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                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Conservative
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boot C,
Wright AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-215262/28.
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Best Local Similarity
Matches 3; Conserv
        Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AA;
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03-DEC-1993;
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1 GYWI 4
                                            2 YWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakey DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                   AAR76079;
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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rheumation, atopic dermatitis, allergic diseases, skin diseases (e.g. skin inflammation, atopic dermatitis and psoriasis), inflammatory diseases out as inflammatory joint diseases (chronic arthritis), inflammatory creal diseases and sinflammatory bowel diseases and graft versus host and transplant rejections. The present sequence is murine Mc-1 antibody heavy, chain variable domain (VH) complementarity determining region 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                 skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; murine; CDR1; heavy. chain variable domain; VH; complementarity determining region 1;
                                  Chemokine construct; human immunodeficiency virus 1; allergic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Murine MC-1 antibody heavy chain variable domain (VH) CDR1 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody; scFv; antibody engineering; antitumour; tumour antigen binding; cytotoxic T-lymphocyte; cell targeting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 23; Length 4;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 116; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Spring M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR85499 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.7%;
larity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-EP10433
                                                                                                                                                                                                                                                                                                                               08-SEP-2000; 2000EP-0119694
05-SEP-2001; 2001US-0948004
                                                                                                                                                                                                                                                                                                                                                                                                                        Mack M, Schloendorff D,
                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROMET AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-362240/39.
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es 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ScFv(FWP51) CDR1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA;
                                                                                                                                                                                                                    WO200220615-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1996
                                                                                                                                                                                                                                                         14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YWWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CDR1)
                                                                                                                                                                                    Mus sp.
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DE19739685-A1.
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2 YWMT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-1999.
                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                           AAW93474;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colitis
                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                               Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components of the heavy chain variable region and light chain variable region, respectively, of single chain antibody scFv(FWP51) (AAR85495). The CDRs are derived from mouse monoclonal antibody FWP51 (ECACC 90112118) directed to the human growth factor receptor HBR2. The scFv is used as the tumour antigen binding domain of a bifunctional protein that is expressed in cytotoxic T-lymphocytes (CTLs), allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; complementarity determining region; CDR; heavy chain; rat; CEA; rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              New bifunctional proteins for use in killing tumour cells - contg. tumour antigen binding domain, a hinge region and a zeta chain derived from a T-cell antigen receptor
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                                                                                                                                                                                                                                                                                                                      Score 24; DB 16; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
monoclonal antibody; cancer; adoptive immunotherapy; complementarity determining region; CDR.
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                                                                                                                                                                                                Disclosure; Page 6; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                AAW23429 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                     adoptive immunotherapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansen H, Leung S, Losman MJ;
                                                                                                                                                                                                                                                                                                                      72.7%;
larity 75.0%;
Conservative 1
                                                                                             94EP-0810244.
                                                                            95WO-EP01494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDR-1 of rWI2 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; idiotype region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-{ IMMUNOMEDICS INC.
                                                                                                             CIBA ) CIBA GEIGY AG.
                                                                                                                              Moritz D;
                                                                                                                                              WPI; 1995-393085/50.
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                      5 AA;
                                                                           20-APR-1995;
                                                                                           02-MAY-1994;
                                         WO9530014-A1
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                                                          09-NOV-1995
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                                                                                                                              Groner B,
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                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW23429;
                                                                                                                                                                                                                                                                                                      Sequence
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This sequence represents the complementarity determining region-1 (CDR-1) of the rWI2 heavy Chain. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotype antibody of the invention is a chimeric or humanised anti-idiotype antibodies (cAb and hAb, respectively) or a fragment which sepcifically binds to the idiotype region of an anti-carcinoembryonic antigen (CBA), where: (i) cab comprises the rWI2 light (I) and heavy (H) chain variable regions, or silent mutations, and (ii) hAb comprises rWI2 complementarity determining regions (CBR) and humanised framework (FR) regions. The hAb is used as a vaccine to stimulate an immune response in a patient against cancers expressing CBA. The hAb, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CBA antibody is used as a (pre-)targeting or therapy agent. The cAb is used to detect the presence of an antibody that specifically binds to CBA in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; hypervariable domain; heavy chain; CDR1; neutralise; Clostridium difficile; epitope; ligand domain; immunotherapy; disease; translocation domain; catalytic domain; humanised antibody; enterotoxin; toxin A; toxin B; pseudomembranous colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                      Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mAk TTC8 hypervariable domain heavy chain CDR1 protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 24; DB 18;
75.0%; Pred. No. 7.8e+05;
iive 1; Mismatches 0;
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                                                                                                                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 8; 14pp; German
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es 3, Conservative
                                                                                                                                                                                                                                                 Claim 3; Page 30; 46pp;
WPI; 1997-479997/44.
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N-PSDB; AAX23235.
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Gaps

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This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist antibody or a pharmaceutical composition comprising the antibody is useful for treating or preventing an infectious disease state such as bacterial infection, viral infections, sepsis, antibiotic resistant bacterial infection, viral infections and those involving intracellular pathogens and parasites such as Listeria monocytogenes, Salmonella and lesishmania in a mammal. Nucleic acid sequences encoding the variable light chain and heavy chain peptide sequences are useful for mutagenic introduction of specific changes within the nucleic acid sequences encoding the (complementarity determining regions) CDRs or framework and for incorporation of the resulting modified or fusion nucleic acid sequence into a plasmid for expression. The CDR-encoding regions comprising silent mutations are used in construction of humanized
This invention describes a novel monoclonal antibody that is directed against. a Clostridium difficile toxin and recognises and neutralises an epitope in the ligand domain, translocation domain or catalytic domain of the toxin. Humanised antibodies are desribed which are expressed in plants and can be used for immunotherapy of diseases caused by Clostridium difficile enterotoxin (toxin A) or cytotoxin (toxin B), especially pseudomembranous colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sialoadhesin factor-1 agonist antibody having the characteristic of monoclonal antibody 13G3 or 11G4 for treating osteomyelitis, deep seated wound infections and antibiotic resistant bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sialoadhesin factor-1; SAF-1; anti-SAF-1 wonoclonal antibody; 13G3; 11G4; osteomyelitis; wound infection; sepsis; Listeria monocytogene; Salmonella; Leishmania; heavy chain variable region; mouse; complementarity determing region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-SAF-1 antibody 13G3 H chain V region CDR peptide SEQ ID 3.
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                                                                                                                                                                                                    Score 24; DB 20; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAB62861 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erickson-Miller CL, Holmes SD,
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                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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                                                                                                                                                               5 AA;
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating or preventing immunoglobulin-mediated reperfusion or ischemic injury resulting from e.g. angioplasty or bypass surgery, by administering an inhibitor of pathogenic immunoglobulin and ischemic antigen interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                 Gaps
antibodies or other engineered antibodies. The present sequence represents anti-SAF-1 monoclonal antibody 13G3 heavy chain variable region complementarity determining region peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin, Ig; reperfusion; ischaemic injury; pathogenic; CDR;
vasotropic; antibody; 22A5; IgM; complementarity determining region.
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                Score 24; DB 22; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               22A5 IgM heavy chain variable region CDR1 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 54; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                               ABB07357 standard; peptide; 5 AA
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75.0%;
                                                                                                72.7%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                 (first entry) .
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Best Local Similarity 75.00
Lag 3; Conservative
                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BLOO-) CENT BLOOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-139643/18.
N-PSDB; ABA94514.
                                                                                                              Local Similarity
tes 3; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         H-CDR-1 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                    Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
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                                                                                                      AAR74929 standard; peptide; 5 AA.
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Search completed: April 22, 2003, 13:39:53 Job time : 35 secs 2 YWM 4 2 YWM 4 ઠે g

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Sequence 1, Appl
Sequence 40, Appl
Sequence 40, Appl
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Sequence 265, App
Sequence 1, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 62, Appl
Sequence 62, Appl
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Sequence 61, Appl
Sequence 23, Appl
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Sequence 31, Appl
Sequence 3, Appli
Sequence 15, Appl
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                                                                                                                                                                                                                                        April 22, 2003, 13:41:42 ; Search time 15 Seconds (without alignments) 26.710 Million cell updates/sec
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1: \( cgn2 \) \( cpr\) \( cp
GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-58-794-23

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US-09-750-754-15
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 88, Appli
Sequence 15, Appli
Sequence 194, Appl
Sequence 11, Appl
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 95, Appli
Sequence 95, Appli
Sequence 96, Appli
Sequence 96, Appli
Sequence 80, Appli
Sequence 81, Appli
Sequence 81, Appli
Sequence 81, Appli
Sequence 29, Appli
Sequence 81, Appli
Sequence 81, Appli
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Sequence 29, Appli
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Sequence 24, Appl
Sequence 8, Appli
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Sequence 58, A
Sequence 74, A
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Sequence 58,
                              US-09-982-172-194
US-09-929-924-41
US-09-929-924-41
US-09-92-172-194
US-09-921-417-38
US-10-165-015-10
US-09-977-811-10
US-09-977-811-10
US-09-778-006-95
US-09-788-006-95
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US-09-952-768-69
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US-09-758-198-58
US-09-185-908-24
US-10-119-537-8
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APPLICANT: Watkins, Jeffrey D.
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Wu, Herren
APPLICANT: Wu, Herren
TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
FILE REFERENCE: AME-06805
CURRENT APPLICATION UNMBER: US/09/977,797A
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-04
NUMBER: OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Patent No. US20010049829A1;
GENERAL INFORMATION:
APPLICANT: BURIFIEL CALL.
ITILE OF INVENTION:
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
; Sequence 76, Application US/09977797A; Publication No. US20030044772A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-968-561A-265

US-09-968-561A-265

Sequence 265, Application US/09968561A

Sequence 265, Application US/09968561A

Sequence 265, Application US/09968561A

Sequence 265, Application US/09968561A

SEXEMATION: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT PILING DATE: 1997-10-01

PRIOR APPLICATION NUMBER: US 60/065,248

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-21

PRIOR PILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-24

PRIOR PILING DATE: 1997-11-21

PRIOR PILING DATE: 1997-11-3

PRIOR PILING DATE: 1997-11-3

PRIOR PILING DATE: 1997-11-3

PRIOR PILING DATE: 1997-11-21

SETUR APPLICATION NUMBER: US 09/511,939

PRIOR FILING DATE: 1998-10-20

PRIOR PILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 350

SOFTWARE: Patentin Version 3.1
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SEQUENCE 1, Application US/09155106

PUBLICATION NO. US20030054003A1

GENERAL INFORMATION:

TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106

FILING DATE: 19-MAR-1997

PRIOR APPLICATION NUMBER: US 60/013,708

FILING DATE: 19-MAR-1996

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids
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                                         Length 5;
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                                         Score 27; DB 10; 1
Pred. No. 2.7e+05;
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Pred. No. 2.7e+05;
                   81.8%; Scc...
100.0%; Pred. No. 4...
0; Mismatches
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80.0%;
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Best Local Similarity 80.0-
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-265
                            Query Match
Best Local Similarity
Matches 4; Conserval
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1 GYYMS 5
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US-09-155-106-1
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APPLICANT: HANSEN, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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COUNTRY: USA
ZIF: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION OF COMPANIES APPLICATION OF CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 27; DB 10; Length 5; 100.0%; Pred. No. 2.7e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-02-14
PRIOR PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 61
LENGTH: 5
LENGTH: 5
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
U8-09-253-794-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09253794
Patent No. US20020018750A1
GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-832-312-61
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US-09-253-794-23
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GENERAL INFORMATION:

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Huse, William D.

APPLICANT: Wu, Herren

TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

FILE REPRENCE: AME-06805

CURRENT APPLICATION NUMBER: U9/09/977,797A

CURRENT FILING DATE: 1998-004

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 136

SOFTWARE: PALENTIN VUMBER: 08/05.825

SEQ ID NO 90

LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; • OTHER INFORMATION: Amino acid sequence of CDR(1) of H chain V region of J OTHER INFORMATION: mouse anti-HM 1.24 antibody US-09-269-921-6
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                                                                                                                                                                                  Sequence 6, Application US/09269921
; Bequence 6, Application US/09269921
; Publication No. U320030045691A1
; GENERAL INFORMATION:
    APPLICANT: Onton, Koichiro
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimara, Yasushi
; APPLICANT: Koishimara, Yasushi
; APPLICANT: MUNGHER: US/09/269,921
CURRENT APPLICATION NUMBER: US/09/269,921
; EARLIER APPLICATION NUMBER: UP 8-264756
; EARLIER FILING DATE: 1996-10-04
; BARLIER FILING DATE: 1996-10-04
; SEQ ID NOS: 137
; SEQ ID NOS: 137
; SEQ ID NOS: 137
           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.7%; Score 23; DB 9; Length 5; 100.0%; Pred. No. 2.7e+05; ive 0; Mismatches 0; Indels
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        Mismatches
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Best Local Similarity 75.03
Matches 3; Conservative
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        Conservative
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CORGANISM: Homo sapiens
US-09-977-797A-90
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Best Local Similarity
Matches 3; Conserv
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ORGANISM: murine
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US-09-269-921-6
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Patent No. US20020068276A1

GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Lan
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REPRENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                   Length 5;
                                                                                                                                 Score 24; DB 9;
Pred. No. 2.7e+05;
1; Mismatches 0
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APPLICANT: SATO, KOH
APPLICANT: SATO, KOH
TITLB OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1997-05-15
PRIOR PLING DATE: 1997-05-15
PRIOR PLING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATON NUMBER: UP 194445/1997
PRIOR PLING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATON NUMBER: UP 19445/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62, Application US/09423800 Patent No. US20020165363A1
                                                                                                                                   72.7%;
75.0%;
                                                                                                                               Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Matches 4; Conservative
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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1 GYYMS 5
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US-09-192-854-151
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US-09-423-800-62
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US-09-155-106-1
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Sequence 1, Application US/09770002

Sequence 1, Application US/09770002

Patent No. US20020110558A1

GENERAL INFORMATION:

APPLICANT: Peter Lloyd Amlot

APPLICANT: Max H. Schreier

APPLICANT: Max H. Schreier

TITLE OF INVENTION: Use of CD25 binding molecules in the

TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.

CURRENT APPLICATION NUMBER: US/09/770,002

CURRENT APPLICATION NUMBER: US/09/770,002

PRIOR APPLICATION NUMBER: PCT/EP99/05316

MANDER OF THE TENDER FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.7%; Score 23; DB 10; Length 5; 100.0%; Pred. No. 2.7e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 10; Length 5;
Pred. No. 2.7e+05;
1; Mismatches 0; Indels
                GENERAL INPORMATION:
APPLICANT: Busfield et al.
TILLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
SOSTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 5
TYPE: PRT
ORGANISM: mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.7
Best Local Similarity 75.0
Matches 3; Conservative
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Matches 3; Conservative
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ORGANISM: Homo sapiens
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2 YWIS 5
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US-09-291-417-40
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                                                                                                RESULT 10
US-10-102-018-62
; Sequence 6.2, Application US/10182018
; Deublication No. US20030049211A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAL SHIVAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
; FILE REFERENCE: PH-1092-PCT
; CURRENT APPLICATION NUMBER: US/10/182,018
; PRIOR APPLICATION NUMBER: JP 2000-03034
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PARENTIN VET. 2.0
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// LOCATION: (1)...(5)

OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
// CTHER INFORMATION: LDP-02
US-09-748-960-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-748-960-12

Sequence 12. Application US/09748960

Patent No. US20010046496A1

GENERAL INFORMATION:
APPLICANT: Brettman. Lee R.
APPLICANT: Brettman. Lee R.
APPLICANT: Brettman. Lee R.
APPLICANT: Brettman. Lee R.
APPLICANT: Allison, David Edward
ITLE OF INVERTION: Method of Administering an Antibody
ITLE OF INVERTION: Method of Administering an Antibody
ITLE OF INVERTION WIMBER: US/09/748,960

CURRENT FILING DATE: 2000-12-27

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.7%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 3; Conservative 0; Mismatches
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US-09-832-312-49
; Sequence 49, Application US/09832312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-018-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conservat
YWMS 5
                                       2 YWIS 5
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 62
LENGTH: 5
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US-10-029-301-4

Sequence 4, Application US/10029301

Publication No. US20020188107A1

GENERAL INFORMATION:

APPLICANT: Browerda, Christian

APPLICANT: Browerda, Christian

APPLICANT: Peek, Keith

ITLE OF INVENTION: Component of Stem Bromelain (as amended)

FILE REFERENCE: 0623.076002

CURRENT FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US/982,685

PRIOR APPLICATION NUMBER: US/982,685

PRIOR PELING DATE: 1999-08-25

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1997-02-25

PRIOR FILING DATE: 1997-02-25

PRIOR FILING DATE: 1997-02-25

PRIOR FILING DATE: 1997-02-25

PRIOR APPLICATION NUMBER: GB 9703850.9

PRIOR FILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 5
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                                                                                                                                                                                                                                                                                                           60.6%; Score 20; DB 9; Length 5; 100.0%; Pred. No. 2.7e+05; tive 0; Mismatches 0; Indels
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
               CURRENT APPLICATION NUMBER: US/09/291,417A
CURRENT APPLICATION NUMBER: US/09/291,417A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US 60/081,784
HARLIER PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 5
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: April 22, 2003, 13:47:05 Job time : 16 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Ananas comosus
US-10-029-301-4
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserve
                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: CCK4b
US-09-291-417-40
                                                                                                                                                                                                                                                                                                                                                                                                                                1 WMS 3
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2, Appli 39, Appli 2, Appli 2, Appli 14, Appli 11, Appli 12, Appli 13, Appli 14, Appli 13, Appli 14, Appli 14, Appli 16, Appli 17, Appli

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

Perfect score:

Sequence:

OM protein

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Charles C. Ditlow, et al.

TITLE OF INVENTION: ATHEROSCIEROTIC PLAQUE SPECIFIC ANTIGENS,

TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Score 29; DB 2;
Pred. No. 2e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REPERBNCE/DOCKET NUMBER: 7606-053
TELECHONE: (415) 854-3660
TELECHONE: (415) 854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-480-434-22
Sequence 22, Application US/08480434
Partent No. 5811248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: N
US-08-480-434-22
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Sequence 12, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 50, Appl
Sequence 64, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                  April 22, 2003, 13:39:17 ; Search time 28 Seconds (without alignments) 5.254 Million cell updates/sec
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lssued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-08-480-434-31

US-08-480-434-31

US-08-053-451B-32

US-08-244-626-12

US-08-244-626-12

US-08-138-15B-32

US-08-353-451B-32

US-08-353-451B-32

US-08-353-451B-32

US-08-353-451B-32

US-08-353-451B-32

US-08-31B-970B-1

US-08-31B-970B-1

US-08-31B-970B-1

US-08-31B-970B-3

US-08-31B-970B-3

US-08-31B-970B-3

US-08-31B-970B-3

US-08-31B-970B-3

US-08-31B-970B-3

US-08-31B-970B-3

US-08-406-532-5

US-08-308-648-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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US-08-433-613-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                           US-09-674-716B-9
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Match Length
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Sequence 31, Application US/08053451B
Patent No. 595584
GENERAL INFORMATION
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
                                      MEDIUM TYPE: FIPOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESA: 66141 FENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CRARACTERISTICS:
LENGTH: 5 amino acids
TYPE: UNKNOWN
NULECULE TYPE: DNA
WURDCHLETYPE: DNA
WURDCHLETYPE: DNA
WURDCHLETYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-854-3660
TELEFAX: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.9%; Score 29; DB 2;
80.0%; Pred. No. 2e+05;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
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US-08-053-451B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF NUMBER OF SEQUENCES:
ADDRESSED: Pennie & Edmonds
STRER: 1155 Avenue of the Americas
CETY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                               Sequence 31, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Ditlow, et al.
TITLE OF INVENTION: ATTEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 2; Length 5;
Pred. No. 2e+05;
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                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELEFAX: 66141 PENNIE
INFORMATION: 7615) 854-3660
TELEFAX: 66141 PENNIE
INFORMATION FOR SEGO ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-053-451B-22
; Sequence 22, Application US/08053451B
; Patent No. 5955584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: D
HYPOTHETICAL: N
ANTI-SENSE: N
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1 GFWMS 5
                                                                  RESULT 2
US-08-480-434-31
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Gaps
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Patent No. 5al1248

GENERAL INFORMATION:
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY, U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNDER:
TLING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7666-053
TELECOMOVINICATION INFORMATION:
TELECOMOVINICATION INFORMATION:
TELECHORE: (415) 854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 5 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ANTI-SENSE: N
US-08-480-434-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-318-1578-23
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                                                                                                   RESULT 6
US-08-480-434-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Waldmann, Herman
APPLICANT: Waldmann, Herman
APPLICANT: Walsh, Louise
APPLICANT: Crowe, James Scott
APPLICANT: Lewis, Alan Peter
TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: S55 Thirteenth Street, N. W.
CITY: Washington
STATE: D. C.
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

81.8%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         87.9%; Score 29; DB 2; Length 5; 80.0%; Pred. No. 2e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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CUUNTER: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,626
FILING DATE: July 15, 1994
CLASSIFICATION NUMBER: PCT/GB92/0251
FILING DATE: December 4, 1992
CLASSIFICATION NUMBER: PCT/GB92/0251
FILING DATE: December 4, 1992
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: ETENET abrabar aG
REGISTRATION NUMBER: 30,377
RELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
CLASSIFIC CHARACTERISTICS:
CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08244626
Patent No. 5502167
GENERAL INFORMATION:
i INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-31
                                                                                                                                                                                                                                                                                                                                         Query Match 87.9
Best Local Similarity 80.0
Matches 4; Conservative
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US-08-244-626-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYWMS 5
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PACENT NO. 5185431

APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;

HASBGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO

TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR

NUMBER OF SEQUENCE: 31

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/392,841

FILING DATE: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCLUENCE

APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OORNUTER: IBM PC compatible
OORNUTER: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE: 03-085
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-085-1993
FILING DATE: 03-085-1993
FILING DATE: 03-087-1993
FILING DATE: 03-087-1993
FILING DATE: 03-087-1993
FILING DATE: 03-087-1993
FILING DATE: 03-087-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
THORYATH: 5 amino acids
                                                                                                                                                                                       81.8%; Score 27; DB 2; Length 5; 100.0%; Pred. No. 2e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.8%; Score 25; DB 1; 75.0%; Pred. No. 2e+05; cive 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 27, Application US/08353400; Patent No. 5665357; GENERAL INFORMATION:
                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.8
Best Local Similarity 75.0
Matches 3; Conservative
                                           STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-353-400-27
                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                  MOLECULE TYPE: I HYPOTHETICAL: N ANTI-SENSE: N US-08-053-451B-32
                                                                                                                                                                                                                                                                            2 YWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Patent No. 595584

GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO,
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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'o. 2e+05;
0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TELEGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDITOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 26-APR.1993
FILING DATE: 26-APR.1993
FILING DATE: 26-APR.1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 7606-033-999
TELEPHONE: 415-854-3660
TELEPHONE: 415-854-3660
TELEPAX: 415-854-3660
TELEPAX: 415-814-3604
TELEPAX: 415-814-3604
TELEPAX: 6141 PENNIE
INFORMATION POR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acide
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81.8%; Score 27; DB
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 4; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-053-451B-32
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0
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Diskette, 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
GURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
FILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.7%; Score 23; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.7%; Score 23; DB 4; Length 5; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 3; Conservative 0; Mismatches 0; Indels
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Fatent No. 6365154
GREERAL INFORMATION:
APPLICANT: Connie L. Erickeon-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITE REPERENCE: P50843
CURRENT FILING DATE: 1999-09-27
FILE REPERENCE: 1999-09-27
FRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
ILENGTH: 5
TYPE: PRT
CREENT: STEPHENCE
CORRENT: STEPHENCE
CORR
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CTHER INFORMATION: hypervariable region
US-08-318-970B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRATURE:
NAME/KEY: SITE
LOCATION: (1)...(5)
CYTHER INFORMATION: 15B8 heavy chain CDR 1
US-09-406-532-5
JAKET: 413 N. Washington Street CITY: Alexandria STATE: Virginia COUNTRY: Heaven 27.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YWM 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-319-970B-1
IS-Gequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
SEGUENCE 1 INCOMMATION:
TITLE 0F INVENTION: AMTINODES AGAINGT NATI-CHOCKE HUMAN MONOCLONAL
TITLE 0F INVENTION: AMTINODES AGAINGT NATI-CHOCKE HUMAN MONOCLONAL
TITLE 0F INVENTION: AMTINODES AGAINGT NATI-CHOCKE HUMAN MONOCLONAL
TITLE 0F INVENTION: AMTINODES AGAINGT NATI-CHOCKE
SEQUENCES: 46
CORRESPONDERS: 140
CORRESPONDES: 140
CORRESPONDES: 140
CONTRY: USA
STATE: Virginia
CONTRY: USA
ZIP: 2334
COMPUTER REMANALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CONTRY: USA
ZIP: 2334
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
CORREATING SYSTEM: MS DOS 3.1
APPLICATION NUMBER: 26,58
RESERVES POLOCKET NUMBER: 26,588
RESERVENCE POLOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-118-970B-3

Sequence 3, Application US/08318970B

Sequence 3. Application US/08318970B

Patent No. 5589573

GENERAL INFORMATION:

APPLICANT: Hideaki HAGIWARA, et al.

TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC

TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN WONCCLONAL ANTIBODY

TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

MUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Office of Sherman and Shalloway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                       0;
                                                                                                               Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 5; 2e+05; indels
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Best Local Similarity 100.0%; Pred. No. 2e+
Matches 3; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: hypervariable region US-08-318-970B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                     GYW 3
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZID: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLESSIFICATION STEMPA1
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEFRAN: (703)836-9300
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: 4 amino acids
TUBNGTH: 4 amino acids
TUBNGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 1;
Pred. No. 2e+05;
1; Mismatches
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ilarity 66.7%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 2; Conserv
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Sequence 21, Application US/07869933
Setent No. 5770396
PAPELICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: HARDORDORY THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: HAMDNOGLOBULIN
TITLE OF INVENTION: HAMDNOGLOBULIN
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                 US-UB-4/7-UBJA-7

Sequence 7, Application US/08479089A

Patent No. 6383487

GENERAL INPORMATION:
APPLICANT: Andot, Peter L.
APPLICANT: Andot, Gunther
APPLICANT: Cammisuli, Salvatore
TITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6383487artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: BIPPY disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLING DATE:
FLING DATE:
PRIOR APPLICATION NUMBER: 07/669,545
FILING DATE:
PRIOR APPLICATION NUMBER: 08-5EP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 1100-7617
REGISTRATION NUMBER: 100-7617
TELECOMMUNICATION INFORMATION:
TELEFAN: (908) 522-6924
TELEFAN: (908) 522-6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Conservative
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Matches 3; Conserv
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US-07-869-933-21
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                                              2 YWM
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Gaps ; 0

Length 4; 0; Indels

GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd. Copyright

OM protein - protein search, using sw model

April 22, 2003, 13:46:48; Search time 14 Seconds Run on:

(without alignments)
130.468 Million cell updates/sec

US-09-674-716B-11 98 Perfect score:

1 EIRLKSDNYATHYAESVKG 19 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

3433

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cat gene leader pe chloramphenicol O-Ig H chain V-D-J r T-cell receptor be Ig H chain V-D-J r leukotriene B-4 12 neuropeptide pep -flt3 ligand isofor 24K antigen - Myco formaldehyde dehyd formate dehydrogen protein QA100044 amino-acid racemas trypsin (EC 3.4.21 T-cell receptor be protein kinase GSK Ig H chain V-D-J r urease (EC 3.5.1.5 T-cell receptor be Ig heavy chain CRD receptor be aminotransferase c hypothetical prote CD33 antigen homol lacz/IS1 mutant fu Ig heavy chain CRD cytochrome-c oxida protein-disulfide Description -cell SUMMARIES F49215 PQ0072 A41077 S30494 B24362 PH1471 A29520 A61334 PH0768 I56393 PH1631 B60278 **S39387** S59495 PH1587 Query Match Length DB Score Result Š.

ribulose-bisphosph	hypothetical prote	Ig H chain V-D-J r	Ig H chain V-D-J r	hypothetical prote	Ig H chain V-D-J r	Tha p 1 - Thaumeto	26K kidney and gal	leucosulfakinin-II	ranatachykinin B -	leucosulfakinin II	hypothetical prote	hypothetical prote	proteinase E - bla	Iq qamma-2b chain	serine proteinase
\$17217	S51610	PH1622	PH1589	C85956	PH1621	A59396	D58501	GMROL2	B61033	B60656	G64003	D28551	A34858	C30503	PN0125
7	~	N	~	N	N	~	N	н	N	~	C3	N	N	N	N
16	16	16	16	17	18	18	16	10	10	10	12	12	12	12	13
4.	4.	4.	4.	4.	4.	4.	o.	4.	4.	4.	4.	4.	4.	4.	4.
20	20	20	20	20	20	50	13	13	13	19.4	13	13	13	13	19
20	20	20	20	20	20	20	19.5	19	19	19	19	19	19	19	19
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

A39109

hypothetical protein 1 - hepatitis C virus C,Species: hepatitis C virus C,Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1993

C. Accession: A33109
R. Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-R. Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-R. Han, J.H.; Agracterization U.S.A. 88, 1711-1715, 1991
A; Reference number: A39109; MUID:91156678; PMID:1705704
A; Ascession: A39109
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-16 <- HAN>

A; Cross-references: GB:M58406

Gaps ï 27.0%; Score 26.5; DB 2; Length 16; 70.0%; Pred. No. 5.4e+02; Live 0; Mismatches 2; Indels 7; Conservative Best Local Similarity Matches 7; Conserv Query Match

;

8 NYCLH-AESV 16

cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)
C.Species: Thunnus obesus (bigeye tuna)
C.Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C.Accession: S77990

C;Accession: \$77990 R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, submitted to the Protein Sequence Database, June 1997

m

A;Reference number: S77980 A;Accession: S77990

A Molecule type: protein
A, Residues: 1-10 <ARN>
A, Experimental source: heart; liver
C, Genetics: A, Genome: nuclear
C, Function:

A; Pathway: oxidative phosphorylation; respiratory chain C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Gaps .; 0 h 25.5%; Score 25; DB 2; Length 10; Similarity 80.0%; Pred. No. 5.6e+02; 4; Conservative 1; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserv

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formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atlan C, Species: Gadus morhua (Atlantic cod)
C,Species: Gadus morhua (Atlantic cod)
C,Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1996
C,Accession: D46285
R,Danielsson, O.; Jornvall, H.
Proc. Natl. Acad. Sci. US.A. 89, 9247-9251, 1992
A,Title: "Enzymogenesis": classical liver alcohol dehydrogenase origin from the glutathic A,Reference number: A46285, MUID:93028441; PMID:1409630
A,Accession: D46285
A,Accession: D46285
A,Status: preliminary
A,Molecule type: protein
A,Residence extracted from NCBI backbone (NCBIP:116272)
C,Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S59495
R;Friedebold, J; Mayer, F; Bill, E; Trautwein, A.X.; Bowien, B.
Bil. Chem. Hoppe-Seyler 376, 561-568, 1995
A;Title: Structural and immunological studies on the Goluble formate dehydrogenase from / A;Reference number: S59492; MUID:96145736; PMID:8561915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein QA100044 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession PA0046; PA0042
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 2; Lengtn 10;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
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44.4%; Pred. No. 2.5e+03;
rative 2; Mismatches 3; Indels
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83.3%; Pred. No. 2.7e+03;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: stem
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A, Accession: PA0046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-14 <FRI>
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A, Status: preliminary
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1 MKIDNIITY
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Best Local Si
Matches 4;
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Matches
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S59495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG H chain V-D-J region (clone B-less 202) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHIG31
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Modecular characterization of transgene-induced immunodeficiency in B-less mice
                                         Cipyente: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999 C;Accession: 539387 #sequence_revision 26-Jul-1996 #text_change 07-May-1999 C;Accession: 539387 **

Biochem. J. 296, 15-19, 1993 **

Biochem. J. 296, 15-19, 1993 **

A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Teference number: 539387; MUID:94071817; PMID:8250835 A;Accession: 839387 A;Molecule type: protein

A;Residues: 1-19 <SUT>
C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24K antigen - Mycobacterium bovis (fragment)
CiSpecies: Mycobacterium bovis
Rifits, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Rifits, T. Sostopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
A;Fitle: Purification and characterization of major antigens from a Mycobacterium bovis
A;Reference number: A60278; MUID:91147217; PMID:190061
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                      Species: Oryctolagus cuniculus (domestic rabbit)
Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999
Accession: S39387
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.8e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     h Similarity 62.5%; Score 24; DB 2; Length 19; Similarity 62.5%; Pred. No. 1.6e+03; 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
protein kinase GSK-3-beta (EC 2.7.1.-) - rabbit (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-15 c.LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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50.0%;
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Best Local Similarity 50.03
Matches 4; Conservative
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Best Local Similarity
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A;Molecule type: protein
A;Residues: 1-16 <FIF>
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Matches 5; Conserv
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cargonic leader peptide - Streptococcus agalactiae plasmid pIP501
C;Species: Streptococcus agalactiae
C;Species: Streptococcus agalactiae
C;Species: Streptococcus agalactiae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 24-Sep-1999
C;Accession: 830494
R;Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.
R;Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.
A;Tritle: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept
A;Reference number: JQ1950; MUID:93096867; PMID:1461942
A;Accession: 830494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: B24362
R,Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A;Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pUB11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-disulfide reductase (glutathione) (BC 1.8.4.2) Q-5 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Un-1992 #text_change 23-Jun-1993
C;Date: 12-Un-1992 #sequence_revision 12-Jun-1992 #text_change 23-Jun-1993
C;Accession: A41077
R;Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.
J. Biol. Chem. 266, 20337-20344, 1991
A;Title: Purification and characterization of a new isozyme of thiol:protein-disulfide aftic phospholipase C form 1A.
A;Reference number: A41077; MUID:92041865; PMID:1657921
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C.Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 11-May-2000
                                                                                                                                                          Gaps
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A,Residues: 1-9 <TRI>
A,Cross-references: EMBL:X65462; NID:g49071; PIDN:CAA46454.1; PID:g581554
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                                                                                       Length 18;
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Pred. No. 3.4e+03;
1; Mismatches 2; Indels
                                                                                                                                                   4; Indels
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                                                                             22.4%; Score 22; DB 2; I
38.5%; Pred. No. 3.2e+03;
tive 2; Mismatches 4;
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57.1%;
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                                                                                                                                                       Conservative
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A,Molecule type: protein
A,Residues: 1-19 <SRI>
C,Keywords: oxidoreductase
                                                                                                                                                                                                                      6 SDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                     4 SDDY--HFGPGTK 14
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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12 LKKSNFA 18
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              C;Keywords: receptor
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Best Local Si
Matches 3;
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C;Accession: F49215
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
R;Turbett, G.R.; Horne, R.; Mee, B.J.
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, 
                                                                                                                       167525

CD33 antigen homolog - mouse (fragment)

CJ5peciess: Mus gp. (mouse)

Cj5peciess: Mus 167525

R;Chies, JA., Lembezat, M.P.; Freitas, A.A.

Bur. J. Immunol. 24, 1657-1664, 1994

A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is I

A;Reference number: 153392; MUID:94298970; PMID:8026526

A;Reference number: Is3392; MUID:94298970; PMID:8026526

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-15 <RES>

A;Residues: 1-15 <RES>

A;Gross-references: GB:S71349; NID:9550037

CjGenetics:

A;Gene: Ig VH7183
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Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Ciscession: PQ0072
Ritanaka, A.; Ishiguro, N.; Shinagawa, M.
Bibanaka, A.; Ishiguro, N.; Shinagawa, M.
A; Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A; Accession: PQ0072
A; Molecule type: mRNA
A; Residues: 1-18 < TAN>
A; Experimental source: T cell
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%; Score 22; DB 2; Length 15; larity 33.3%; Pred. No. 2.7e+03; Conservative 3; Mismatches 3; Indels
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4 RRDHYGSSY 12
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A, Gene: BTB98
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A;Reference number: A24362; MUID:86081739; PMID:3865770
A;Accession: B24362
A;Accession: B24362
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-9 < RBU
A;Cross-references: GB:X02872; NID:g46536; PIDN:CAA26630.1; PID:g581555
C;Comment: Ribosome stalling in the translation of this leader peptide, caused by the eff malation of the chloramphenicol 0-acetyltransferase from a ribosome binding site located C;Genetics:
A;Genome: plasmid
C;Superfamily: unassigned leader peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1. Constitution (wild-type clone 11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1587
S;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Molecula type: DNA
A;Molecula type: DNA
A;Residues: 1-12 <LEV>
A;Residues: 1-12 <LEV>
A;Reseidues: 1-12 <LEV>
A;Reseidues: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                    Ouery Match 21.4%; Score 21; DB 2; Length 9; Best Local Similarity 42.9%; Pred. No. 2.8e+05; Matches 3; Conservative 4; Mismatches 0; Indels
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3 KSEDYSS 9
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us-09-674-716b-11.closed.rsp

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                     OM protein - protein search, using sw model
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April 22, 2003, 13:43:07 ; Search time 25 Seconds (without alignments) 31.522 Million cell updates/sec Run on:

US-09-674-716B-11 98 1 EIRLKSDNYATHYAESVKG 19

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

1015 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descri	P80526 fasciola he		P47733 locusta mig				zea mays	P80432 rattus norv	P82395 litoria ran		P09039 leucophaea		P81358 clostridium	P81037 oncorhynchu				P21794 rattus norv		P81285 mamestra br	Q02006 rhodopseudo	-		-	Q36834 trichophyto					4	m	P27642 bacillus li	P80575 streptomyce
SUMMARIES	ΩI	NEJ2_FASHE	COXO_THUOB	LOSK_LOCMI	LPCA_STAAU	ALRX_PSEPU	RIP_SIRGR	UC21_MAIZE	COXO_RAT	AU32_LITRA	ATPB CANFA	LSK2_LEUMA	TKNB_RANCA	UN37 CLOPA	MILTONCKE		RL6_VIBPR	EFG_THEAQ	HI70_RAT	TKN_KASSE		YAA3_RHOPA	HTPG_ACICA	AU31_LITRA	- 1	NU4M_TRIRU	FIBB_LAMGL	OXLA_OPHHA	PHLC_STAIN	RR16_GINBI		- 1	SP51_BACLI	AROF_STRRM
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34 17 17.3 19 1 LPRM STRAU P03063 staphylococ 36 17 17.3 19 1 TX3 PHONI P81010 phoneutria 96 17 17.3 19 1 UP24 UPEIN P82030 upercleia i 97 16 16.3 8 1 AL18 CARMA P81821 carcinus ma 98 16 16.3 10 1 GANI PETMA P04378 serwinia chr 90 16 16.3 10 1 TKNB_CHICK P41869 callibhora 97 16 16.3 12 1 PARI_CALVO P91865 gallus gall 97 16 16.3 12 1 PARI_CALVO P90662 physiconitre 98 16 16.3 13 1 AU11_LITRA P82050 litoria ran 98 16 16.3 13 1 AU11_LITRA P82050 litoria ran 98 16 16.3 15 1 CKALOGE P82050 litoria chr 98 16 16.3 15 1 CKALOGE P82050 litoria chr 98 16 16.3 15 1 CKAL_CONGE P82050 litoria chr 98 16 16.3 15 1 CKAL_CONGE P82050 litoria chr 98 16 16.3 15 1 CKAL_CONGE P82050 litoria chr 98 16 16.3 15 1 CKAL_CONGE P82050 litoria chr 98 16 16.3 15 1 CKAL_CONGE	ALIGNMENTS	RESULT 1 NBJ2 FASHE 1D NBJ2 FASHE STANDARD; PRT; 14 AA.			proceins. Biochem!- DEVEL	SEQU	Query Match 27.6%; Score 27; DB 1; Length 14; Best Local Similarity 62.5%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	7 DNYATHYA 14 	COXO_THUOB  COXO_THUOB  COXO_THUOB  COXO_THUOB  COXO_THUOB  COXO_THUOB  COXO_THUOB  COXO_THUOB  Tol-NOV-1997 (Rel. 35, Created)  Tol-NOV-1997 (Rel. 35, Last sequence update)  DT
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21.4%;
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EMBL; X02872; CAA26630.1; -.
EMBL; X60827; CAA43217.1; -.
EMBL; X65462; CAA46454.1; -.
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                                                                                                                                                                                                                                                                               Staphylococcus aureus.";
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Best Local Similarity
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KSEDYSS 9
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-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome c + 2 H(2)0.
-!- SIBLELLULAR LOCATION: Mitochondrial inner membrane.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
OXIGOTEGUCIASE; Inner membrane; Mitochondrion.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoldea; Acrididae; Oedipodinae; Locusta.
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Streptococcus agalactise.
Plasmid pSCS6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI TaxID=1280, 1311;
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Pred. No. 1.7e+02;
1; Mismatches 0; Indele
                                                                                                                                                                                                     Length 10;
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AMIDATION.
9B5B5DA9BD6B5AAA CRC64;
                                                                                                                                                              10 AA; 1059 MW; 126DE767687B1DCB CRC64;
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Pred. No. 6.7e+02;
2; Mismatches 1;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-GCT-1994 (Rel. 30, Last annotation update)
Chloramphenicol resistance leader peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                   12 AA.
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57.1%;
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1 QLASDDY 7
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01-FEB-1996 (
15-DEC-1998 (
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01-JUN-1994
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P47733;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=93096867; PubMed=1461942;
Tribur-Cuot P., de Cespedes G., Horaud T.;
"Nucleotide sequence of the chloramphenicol resistance determinant of the streptococcal plasmid pIP501.";
Plasmid 28:272-276(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=86081739; PubMed=3865770;
Bruckner R., Mataura H.;
"Regulation of the inducible chloramphenicol acetyltransferase gene
of the Staphylococcus aureus plasmid pUB112.";
EMBO J. 4:2295-2300(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence and structural relationships of a chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
SEQUENCE FROM N.A.
SPECIES-S.aureuB; STRAIN=436; PLASMID=pSCS7;
SPECIES-92027652; PubMed=1929326;
Schwarz S., Cardoso M.;
"Nucleotide sequence and phylogeny of a chloramphenicol accetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Broad-specificity amino acid racemase (EC 5.1.1.-) (Fragment).
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Pseudomonas.
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                                                                                                                                                                                                                                                 Antimicrob. Agents Chemother. 35:1551-1556(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 1; 1
Pred. No. 1.1e+05;
4; Mismatches 0;
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Leader peptide; Antibiotic resistance; Plasmid.
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                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.aureus; PLASMID=pSCS6;
MEDLINE=92388047; PubMed=1517170;
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18 AA

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB-Coleoptile;
Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Perrollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELIANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
-!- SIMILARITY: TO L.ASCORBATE PEROXIDASES.
Maize-2DPAGE; P80627; COLEOPTILE.
                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
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Zea mays (Maize)
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P80627
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                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribosome-inactivating protein momorgrosvin (rRNA N-glycosidase) (EC 3.2.2.2) (Fragment).
Siraitia grosvenorii (Monk's fruit) (Luo han guo).
Siraitia grosvenorii (Monk's fruit) (Luo han guo).
Sprantophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Siraitia.
                                                                                                                                                                                                                                                                                                                                                           CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
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"Isolation and characterization of a new ribosome inactivating
protein, momorgrosvin, from seeds of the monk's fruit Momordica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 1.5e+03;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                      Isomerase, Pyridoxal phosphate.
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ACT_SITE 6 CA
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66.7%;
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ilarity 66.7%;
Conservative
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Matches 4; Conserv
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16
16 AA;
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Matches 4; Conserv
                          STRAIN=AKU 0813;
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P83323;
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Score 21, DB 1; Length 18; Pred. No. 1.5e+03; 0; Mismatches 3; Indels

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EUT. J. Biochem. 230:235-241(1995).

EUT. J. Biochem. 230:235-241(1995).

-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONEIAL ELECTRON TRANSPORT.

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                                                                                                         STRAIN=Wistar; TISSUE=Liver, and Heart;
MEDLINE=95324529; PubMed=7601105;
Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
"Cytcohrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
                                                                                                                                                        Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide VIIc, mitochondrial (BC 1.9.3.1)
(VIIIA) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
10 AA.
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Electrophoresis 18:2795-2802(1997)
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Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-APPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                 TISSUE-Granular dorsal gland;

MEDLINE-20408845; PubMed-10951191;

Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,

Razlace J.C., Tyler M.J.;

"The antibiotic and anticancer active aurein peptides from the australian bell frogs Litoria aurea and Litoria raniformis the solution structure of aurein 1.2.";

Eur. J. Biochem 267:5330-5341(2000).

-!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST L.LACTIS, L.INNOCUA,

M.LUTEUS, S. AUREUS, S. ENDERMIDIS AND S.UBERIS. PROBABLY ACTS

DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Canis.
                                                                                                                                                                                                 Litoria raniformia (Southern bell frog), and
Litoria aurea (Green and golden bell frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment)
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                                                                                                                                                                                                                               Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 1; Length 17; Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                      Score 20; DB 1; Length 10;
Pred. No. 1.2e+03;
1; Mismafches 1; Indels
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F6AC0A580428EAFD CRC64;
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae,
NCBI_TaxID=9615;
    1117 MW; 126DE767687B1B0B CRC64;
                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aurein 3.2.
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-1- SUBCELLULAR LOCATION: SECRETED.
Amidation; Antibiotic.
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                       20.4%;
ilarity 60.0%;
Conservative
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                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dog heart proteins.";
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Best Local Similarity
Matches 4; Conserv
                         Query Match
Best Local Similarity
      10 AA;
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TISSUE=Heart;
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SUBUNIT.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: F-TYPE MAIN SUBUNITS: A, B AND C.
-!- SUBUNITS: A, B AND C.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
-!- SIMILARITY: DOCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                         InterPro; IPR000194; ATPase a/bcentre.
PROSITE; PS00152; ATPASE ALPHA BETA; PARTIAL.
ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
SULFATION (IN L.MADERAE, BUT NOT IN P.AMERICANA).
AMIDATION.
-i- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=L.maderae;
MEDLINE=87048769; PubMed=3778455;
Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
"Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to cholecystokinin and gastrin.";
Biochem. Biophys. Res. Commun. 140:357-364(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB9C163FDC60BB42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 1; I
Pred. No. 2.4e+03;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=P.americana; TISSUE=Corpora cardiaca;
MEDLINE=99137190; PubMed=2615921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last amnotation update)
Leucosulfakinin-II (LSK-II).
Leucophaea maderae (Madeira cockroach), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A26335; GMROL2.
PIR; B60565; B60565.
InterPro; IPRO01651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AA; 1871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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Comp. Biochem. Physiol. 117B:445-452(1997).
-1- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYSES BASIC PROTEINS.
HYDROLYZE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLUPAINE BUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOT MILK CASEIN.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE WITH BASIC RESIDUES AT
                                                                            Plengerud R., Skjeldal L.; Two-dimensional Plengerud R., Skjeldal L.; Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5."; Electrophoresis 19:802-806(1998).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.8, ITS MW IS: 44.7 kba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISI ANAVA STANDARD; PRT; 15 AA.
044507;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Cysteine desulfurase 1 (BC 4.4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifs1) (Fragment).
Anabaena variabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Miltpain, new cysteine proteinase from the milt of chum salmon, Oncorhynchus keta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena
                                                                                                                                                                                                                                                        / Match 19.4%; Score 19; DB 1; Length 14; Local Similarity 41.7%; Pred. No. 2.5e+03; les 5; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.4%; Score 19; DB 1; Length 15; 80.0%; Pred. No. 2.7e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                             NON_TER 14 14 14 SEQUENCE 14 AA; 1579 MW; 05384662DEF89210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 15 15 15 15 AA; 1730 MW; 766B7771C0F888E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Miltpain (EC 3.4.22.-) (Fragment).
Oncorbynchus keta (Chum salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                        STRAIN=W5;
MEDLINE=98291870; PubMed=9629918;
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Kawabata C., Ichishima E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 80.0
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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P81037;
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SEQUENCE
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SEQUENCE.
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MILT ONCKE
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NIS1 ANAVA
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intestine.",
Regul. Pept. 46:81-88(1993).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ranatachykinin B (RTK B).
Rana catesbelaina (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; RanaillaxIII-8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDLINE=91254337; PubMed=2043143;
Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
"Isolation of four novel tachykinins from frog (Rana catesbelana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL.

15-JUL.1998 (Rel. 36, Created)

15-JUL.1998 (Rel. 36, Last sequence update)

15-JUL.1998 (Rel. 36, Last annotation update)

Unknown protein CP 37 from 2D-page (Fragment).

Clostridium pasteurianum.

Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,

Clostridium.
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MEDLINE=94023216; PubMed=8210506;
Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
"Four novel tachykinins in frog (Rana catesbeiana) brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%; Score 19; DB 1; Length 10; 60.0%; Pred. No. 1.7e+03; Live 2; Mismatches 0; Indels
                                        Length 10;
                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR02240; Tachykinin.
PR051TE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation.
MOD RBS 10 10 AMIDATION.
SEQÜENCE 10 AA; 1210 MW; 917E556B59D5BAB5 CRC64;
1255 MW; 9B4F5391E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain and intestine.";
Biochem. Biophys. Res. Commun. 177:588-595(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                    19.4%; Score 19; DB 1; I 60.0%; Pred. No. 1.7e+03; tive 2; Mismatches 0;
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                                                                            Conservative
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les 3; Conservative
                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND SYNTHESIS.
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELOI
PIR; JE0427; JE0427.
PIR; B61033; B61033.
10 AA;
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2 KSDSF 6
                                                                                                               5 KSDNY 9
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UN37 CLOPA
ID UN37 CLOPA
AC P81356;
DT 15-JUL-1998
DT 15-JUL-1998
DT 15-JUL-1998
DC UNKNOWN prott
OC Bacteria; Filo
CC Clostridium;
OC NOST CLOSTRIDIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KSDNY 9
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1 QSDDY :
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SEQUENCE
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TKNB_RANCA
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                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOWDDIMER (BY SIMILARITY).
-!- MISCELLANDEOUS: BELONGS TO THE NIFT (GENE CLUSTER WHICH IS EXPRESSED IN HETEROCYSTS UNDER ANABROBIC CONDITIONS.
-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL STLFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INORGANIC. SULFUR REQUIRED FOR THE FE-S CORE FORWATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                EXPRESSION PATTERN.
STRAIN-PCC 7937 / ATCC 29413;
MEDLINE-96016168; PubMed=7568132;
Thiel T., Lyons E.M., Erker J.C., Ernst A.;
"A second nitrogenase in vegetative cells of a heterocyst-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1; Length 15;
Pred. No. 2.7e+03;
0; Mismatches 1; Indels
                                   SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Monneriahn U., Boehme H.; to the EMBL/GenBánk/DDBJ databases.
Submitted (DEC-1992) to the EMBL/GenBánk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000192; Aminotransfv.
PROSITE; PS00595; AA_TRANSFER CLASS 5; PARTIAL.
Nitrogen fixation; Lyase; Pyridoxal_phosphate.
15 15
SEQUENCE 15 AA; 1684 MW; 08B8F106DE65547D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%;
80.0%;
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Best Local Similarity
Matches 4; Conserv
NCBI_TaxID=1172;
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Search completed: April 22, 2003, 13:48:59 Job time: 27 secs

7 DNYAT 11 || || 7 DNNAT 11

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Q8upi2 human immun Q9r4h9 bordetella

Q9uwj7 archaecglob Q9pxx1 struthio ca Q9x1p pseudomonas Q9x4p pseudomonas Q9x73 drosophila Q9x73 drosophila Q9xff bos taurus Q9xff bos taurus Q9xff bos caurus Q5672 yersinia pe G60842 homo sapien Q9uwl pyrococcus. P8346 aaaphis dic Q9tr18 sus scrofa Q9tr18 oryctolagus Q9tr18 cryctolagus Q9tr20 mus musculu Q5210 staphylococ Q9737 escherichia Q9737 escherichia

Sequence:

Run on:

Searched:

Ogqux0 mus sp. tum O53545 shigella so O9trf7 oryctolagus Q43370 allium cepa P96305 alteromonas Q54394 streptomyce

bacteriopha

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[1] _
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J.,
Whetsell A.J., Cao Y., Ho D.D., Safrit J.T., Koup R.A.;
"Adaptive Evolution of Human Immunodeficiency Virus Type 1 During the
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 15; Length 19;
Pred. No. 1.5e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A.
STRAIN=SAMPLE P4.25-15;
MCDOMAID D.;
SUDMITTER (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U36027; AAA97722.1; -.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER 1 1 1 SEQUENCE 19 AA; 2066 MW; E117102D52800EF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                   19 AA.
                                                                                                                                                                                                                                                                                      ALIGNMENTS
                         Q9UWJ7
Q9PRX1
Q9R474
Q9R474
Q9R973
Q9V973
Q9C8FF
Q9TRF1
Q9UWH4
P9J246
Q9TRT13
Q9GXTR18
                                                                                                                                                                                                                              Q43370
Q43370
P96305
Q54394
                                                                                                                                                                                                    Q9QUX0
Q53545
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Q47337
Q9TNP1
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                                                                                                                                                                                                                                                                                                                                                                                Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.7%;
50.0%;
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Best Local Similarity 50.v.
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073129
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P33219 homo sapien
Q91bm5 human immun
Q91c27 homo sapien
Q91434 salmonalla
Q91434 caulobacter
Q9146 thermococcu
Q9146 sus scrofa
Q9146 sus scrofa
Q9147 tityus serr
Q93057 homo sapien
P70319 mus musculu
Q9164 heliobacill
P96423 pseudomonas
                                                            April 22, 2003, 13:45:28 ; Search time 28 Seconds (without alignments) 139.818 Million cell updates/sec
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         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                  671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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P83219
Q91BM5
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sp_plant:*
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sp_unclassified:*
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"FLB1, a human protein of epididymal origin that is involved in the sperm-cocyte recognition process.";
Biol. Reprod. 52:267-78(1995).
SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robbe-Saule V., Coynault C., Ibanez-Ruiz M., Hermant D., Norel F.; "Identification of a non-haem catalase in Salmonella and its regulation by Roos (sigma 8)."; Mol. Microbiol. 39:1533-1545(2001).
                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2000 (TrEMBLrel. 14, Last annotation update)
94 kDa epididymal cytokeratin-like protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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NON TER 19 19
SEQÜENCE 19 AA; 2448 MW; 05D3DB83C7CBE7E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 2.4 kDa protein (Fragment).
PUTATIVE YCIE.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
proteolysis tag (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 2;
Pred. No. 1e+03;
13 AA.
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                                                                                                                                                                                                                                        MEDLINE=95226590; PubMed=7536047;
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Matches 4; Conservative
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PRELIMINARY;
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Q9KHJ4;
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Q9UC27
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Q9L434
ID Q9L43
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                                                                                                                                                                                                                   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUE=NASAL MUCUS;
MEDLINE=2141375; PubMed=11522286;
Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
"Calcitermin, a novel antimicrobial peptide isolated from human airway
                                                                                                                                                                                                                                                                                                                                                                IS
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MEDLINE=9115054; PubMed=7815476;
Ahmad N., Baroudy B.M., Baker R.C., Chappey C.;
"Genetic analysis of human immunodeficiency virus type 1 envelope V3
region isolates from mothers and infafits after perinatal
transmission.";
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                                                                                                                                                                                                                                                                                                                 PEGETELIONS.";
FEBS Lett. 504:5-10(2001).
- FUNCTION: POSSESSES ANTIFUNGAL ACTIVITY AGAINST C.ALBICANS AND ALSO ACTIVE AGAINST E.COLI AND P.AERUGINOSA BUT NOT L.MONOCYTOGENES AND S.AUREUS.
- I. MASS SPECTROMERRY: NW-1688.9; METHOD=MALDI.
- MISCELLANEOUS: OPTIMUM PH IS 5.4.
- MISCELLANEOUS: ANTIMUCROBIAL ACTIVITY IS ENHANCED BY ZNCL2.
- SIMILARITY: TO THE C.TERMINUS OF HUMAN CALGRANULIN C.
- SIMILARITY: TO THE C.TERMINUS OF HUMAN CALGRANULIN C.
- Antibiotic; Fungicide; Zinc; Metal-binding.
DOWAIN
SEQUENCE 15 AA; 1689 MW; CE4EC8DDFE861663 CRC64;
                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 4; Length 15;
Pred. No. 2.4e+02;
2; Mismatches 3; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Envelope glycoprotein, V3 region (Fragment).
                                       Created)
Last sequence update)
Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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EMBL; U16595; AAA64161.1; -.
NON TER 1
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                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 54.5
Matches 6; Conservative
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    PRELIMINARY;
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4 EVIIRSDNFS 13
                                                                                                    Calcitermin.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 2.1 kDa protein (Fragment).
unidentified human poliovirus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=92144618; PubMed=1737046;
Koike K., Urata Y., Goto S.;
Proteinsae-catalyzed activation of porcine heart muscle pyruvate dehydrogensse and identification of its cleavage site.";
Biochim. Biophys. Acta 1118:223-230(1992).
SEQUENCE 15 AA; 1757 MW; 9405BFFE4B126598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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"Primary structure of poliovirus defective-interfering particle genomes and possible generation mechanisms of the particles.";
J. Mol. Biol. 192:473-487(1986).
EMBL, M30221; AAA66829.1;
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Pred. No. 1.5e+03;
0; Mismatches 1; Indels
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            dehydrogenase and identification of its cleavage site.";
                                                                                                                                                                                               1, Indels
                                     Biochim. Biophys. Acta 1118:223-230(1992).
SEQUENCE 15 AA; 1787 MW; DB1265CDF7737E16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UIN-2000 (TrEMBLrel. 14, Last annotation update)
Pyruvate dehydrogenase (EC 1.2.4.1) (Fragment).
                                                                                                                                26.5%; Score 26, DB 6; I ilarity 71.4%; Pred. No. 1.1e+03; Conservative 1; Mismatches 1;
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MEDLINE=87169734; PubMed=3031313;
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Matches 5; Conserv
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                                                                                                                                          MEDLINE=20345063; PubMed=10884408;

Keiler K.C., Shapiro L., Williams K.P.;

Keiler k.C., Shapiro L., Williams K.P.;

turkNas that encode proteolysis-inducing tags are found in all known bacterial genomes: A two-piece tmRNA_functions in Caulobacter.";

Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783 (2000).

BMBL; AF255738; AAF87998.1; -...

SEQÜENCE 13 AA; 1368 MW; CE5F60C57FCEIBID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITME=96146528; PubMed=8550513;
Heider J., Mai X., Adams M.W.;
"Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
new and reversible coenzyme A-dependent enzyme involved in peptide
fermentation by hyperthermophilic archaea.";
J. Bacteriol. 178:780-787(1996).
SEQUENCE 15 AA; 1549 MW; 0C1766910B222944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92144618; PubMed=1737046;
Koike K., Urata Y., Goto S.;
"Proteinase-catalyzed activation of porcine heart muscle pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha
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Pred. No. 9.4e+02;
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01-MAY-2000 (TrEMBLrel. 13. Last som
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44.4%;
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Best Local Similarity 45.5
Matches 5; Conservative
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Caulobacter crescentus
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                                                                                    NCBI_TaxID=155892;
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2 NDNFAEEFA 10
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NCBI_TaxID=2265;
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1D 09TRT7
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MEDLINE-56234102; PubMed=8650211;
Busslinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.;
"Deregulation of PAX-5 by translocation of the Emu enhancer of the IgH
                                                                                                                                                                                                                                                                                                                                                                                         Iida S., Rao P.H., Nallasivam P., Hibshoosh H., Butler M., Louie D.C., Dyomin V., Ohno H., Chaganti R.S.K., Dalla-Favera R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96234102; PubMed=8650231; MEDLINE=96234102; PubMed=8650231; Busslinger P.G., Kozmik Z.; Busslinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.; Busslinger M. Klix N., Pfeffer P., Graninger P.G., Kozmik Z.; Busslinger P.G., Kozmik Z.; Decentation of the Emu enhancer of the Iglibergulation of PAX-5 py translocation of the Emu enhancer of the Iglibergulation of PAX-5 py translocation of the Emu enhancer of the Iglibergulation of Iglib
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Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
Hypermutation of multiple proto-oncogenes in B-cell diffuse large-cell lymphomas.";
Nature 412:41-346 (2001).
EMBL; U62539; AAB09533.1; -.
EMBL; AF074013; AAC69188.1; -.
EMBL; AR074013; AAC69188.1; -.
EMBL; AR074013; AAC69188.1; -.
EMBL; AR074013; AAC6918.1; -.
EMBL; AR074013; AAC6918.1; -.
EMBL; AR074013; AAC6918.1; -.
EMBL; AR074013; AAC6918.1; -.
                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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TISSUE=MARGINAL ZONE LYMPHOMA;
Morrison A.M., Jaeger U., Chott A., Haas O.A., Schebesta M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 4; Length 14; Pred. No. 2.2e+03; 2; Mismatches 4; Indels
                                     01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B cell specific activator protein BSAP (PAX5) (Fragment).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marginal zone lymphoma.";
Blood 0:0-0(1998).
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2 EIHCKHDPFAS 12
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                                                                                                                                                 PAXS OR PAX-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and physical mapping of RNA polymerase genes from Methanobacterium thermoautotrophicum and comparison of homologies and gene orders with those of RNA polymerase genes from other Methanogenic archaebacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88198019; PubMed=2834336;
Schallenberg J., Moes M., Truss M., Reiser W., Thomm M., Stetter K.O.,
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Tityus serrulatus (Brazilian scorpion).
Bukaryota; Metazos; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Tityus.
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Ferreira L.A., Alves E.W., Henriques O.B.;
"Peptide T, a novel bradykinin potentiator isolated from Tityus serrulatus scorpion venom.";
Toxicon 31:941-947(1993).
SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;
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01-MAY.2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2002 (TrEMBLrel. 12, Last annotation update)
RNA polymerase subunit B'' (Fragment).
Methanobacterium thermoautocrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 1.9e+03;
1; Mismatches 1; Indels
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Last sequence update)
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EMBL; M20391; AAA72654.1; -.
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9 NYTTH 13
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01-MAY-2000
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locus adjacent to two alternative PAX_5 promoters in a diffuse largecell lymphoma.";
Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
EMBL, U56838; AAB16835.1; -.
NON TER 14 14
SEQÜENCE 14 AA; 1683 MW; E113518FA19953A1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Proteolysis tag (Fragment)
Heliobacillus mobilis
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia, Clostridia, Stanicutes; Heliobacteriaces, Heliobacteri
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24.5%; Score 24; DB 11; Length 14;
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SEQUENCE FROM N.A.
Williams K.P.;
"Phylogenetic analysis of tmRNA.";
"Phylogenetic analysis of tmRNA.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY040838; AAK83526.1; -...
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MEDLINE-20063247; PubMed=10592213;
Williams K.P.;
"The tmRNA website.";
Nucleic Acids Res. 28:168-168(2000).
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2 EIHCKHDPFAS 12
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Best Local Si
Matches 4;
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Search completed: April 22, 2003, 13:49:34 Job time : 30 secs

Human anti-idiotyp Human antibody CAT Llama CDR2 region Llama CDR2 region Heavy chain CDR2 r Human anti-idiotyp Anti-hill2 antibod Human heavy chain Llama CDR2 region Llama CDR2 region

Scoring table:

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Run on:

Mouse antibody var Anti-hIL12 antibod Llama CDR2 region Human anti-HBs ant Llama CDR2 region

H-CDR-2 of anti-id Scaffold protein S Mutant 3 of the CD

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CD23; FCERII; IgE receptor; monoclonal antibody; CII; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erychematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erychematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria, nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy, asthma; rhinitis; czema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain CDR H2 of mouse anti-CD23 MAb C11.
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                                                                                                            AAU82611
AAW90323
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AAU82550
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AAB39868
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 B-cell malignancy; therapy.
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Mus musculus
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 Light chain CDR H2
Murine PSCA antibo
Scaffold protein S
A3 derivative #15,
H. pylori 26 kDa p
CDRH 20 f monoclona
Mouse mAb 1D9 anti
Anti-Staph (HAY) 9
Llama CDR2 region
H-CDR-2 of anti-id
                                                                          April 22, 2003, 13:42:32 ; Search time 73 Seconds (without alignments) 34.682 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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98GB-0009839.

19-MAY-1998;

Score

Result Š. 2645978901

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Anti-platelet glyc Human scFv clone 2 D12 scFv CDR H2 re Anti-TANGO 268 scF Anti-IL-18 antibod

Anti-cancer specif Tumour antigen ant Anti-hILL2 antibod Anti-hILL2 antibod Anti-hILL2 antibod

Mutant 5 of the CD Anti-platelet glyc Mouse HeFi antibod

A3 derivative #16 Llama CDR2 region us-09-674-716b-11.closed.rag

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(CDR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal
antibody C11 (see also AAX32263). The invention provides altered
antibodies, such as chimeric or humanised antibodies, which comprise
cutficient of the amino acid sequences of C11 light and heavy chain
CDRs (see AAX3224-59) to render them capable of binding to the CD23
cype II molecule expressed on haemacopoietic cells. The antibodies
are used to block soluble CD23 formation for treatment of arthritis,
type II molecule expressed on haemacopoietic cells. The antibodies
c are used to block soluble CD23 formation for treatment of arthritis,
clupus exthematous, Hashimoto's thyroiditis, multiple sclerosis,
diabetes, uveitis, dermatitis, inflammatory bowel disease, ulcerative
syndrome, glomerulonephritis, inflammatory bowel disease, allergic
colitis, Crobin's disease, Sjogren's syndrome, allergies, allergic
asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
ccema, graft-versus-host disease, COPD, insultis, bronchitis
charactery are allergies of precision and allergies allergies allergies of particularly chronic bronchitis of disease, COPD, insultis, bronchitis
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                                                                           diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; mouse; prostate cancer;
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   Shearin J;
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 Rapson NT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate stem cell antigen; PSCA; human; diagnosis; treatment; chromosome 8q24.2
Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35297 standard; Peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine PSCA antibody fragment #5.
                                                                                                                                        Claim 1; Page 40; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining the binding agents
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03-MAY-2000; 2000US-0564329
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 Crowe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
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UROGENESYS.
                                 WPI; 2000-053101/04.
N-PSDB; AAZ34743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-159478/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200105427-A1.
Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV
(UROG-) UROGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB35297;
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                                                                          with prostate stem cell antigen (PSCA) by administering an antibody which selectively binds to PSCA and inhibits the growth of the cancer cells. The PSCA gene is found on human chromosome 8Q24.2 The invention provides the human and murine PSCA protein and coding sequences, which can be used not only in the treatment of, but also in detection and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB22930-B2939 were used in the production of the proteins of the invention.
                                                              present invention describes a method of treating cancer associated
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful supporting framework and carrying antigen- or receptor binding
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.6%; Score 80; DB 21; Length 17;
88.2%; Pred. No. 1.2e-06;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                         Score 91; DB 22; Length 19;
Pred. No. 2e-08;
                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scaffold protein SCA A3 peptide SEQ ID NO: 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sablon
                                                                                                                                                                                                                         ch 92.9%; Score 91; DB 1. Similarity 89.5%; Pred. No. 2e-0 17; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoodenboom H,
                                Example 21; Fig 61; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         AAB30033 standard; Peptide; 17
                                                                                                                                                                                                                                                                                                            1 EIRLRSENYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-EP02283
                                                                                                                                                                                                                                                                                         1 EIRLKSDNYATHYAESVKG 19
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Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-665002/64.
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                             19 AA;
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                                                                                                                                                              prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060070-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                           Query Match
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Gaps

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Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
                                                                                                                                                                                                                               New scaffold protein, useful for stabilizing antigens used as vaccines
                                                                                    A3 derivative #15, beta strand of scaffold protein structure.
                                                                                                                                                                                                     Sablon E;
                                                                                                                                                                                                     Hoodenboom H,
                                                                                                                                                                                                                                                   Disclosure; Page 6; 105pp; English.
                                             AAY40694 standard; peptide; 16 AA.
                                                                                                          tumour; chemotherapeutic agent.
                                                                                                                                                              98EP-0870065.
                                                                                                                                                                         98EP-0870065
                                                                        (first entry)
3 RLKSDNYATHYAESVKG 19
        1 RLNSDNFATHYAESVKG 17
                                                                                                                                                                                       (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                     Hufton S,
                                                                                                                                                                                                                  WPI; 1999-542958/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA;
                                                                                                                                                             31-MAR-1998;
                                                                                                                                                                          31-MAR-1998;
                                                                        01-DEC-1999
                                                                                                                                                06-OCT-1999.
                                                                                                                                   EP947582-A1
                                                                                                                      Synthetic.
                                                                                                                                                                                                     Desmet J,
                                                          AAY40694;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                       AAY4069
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All peptides (AAAY6061) which forms part of a seaffold protein. As is a beta strand peptide which forms part of a beta sheet. Peptides (AAAY60605) which forms part of a beta sheet. Peptides (AAAY601-Y4609) which form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed form the beta strands \$1.83, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets \$1/84/83 and \$6/85/82 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands \$1.83 are included in the structure the scaffold is constructed of two beta sheets, with the structure the scaffold is constructed of two beta sheets, with the structure of the additional beta strands \$1.83 are included in the structure to caffold is constructed of two beta sheets, with the structure of the additional beta strands \$1.83 are included in the structure of the additional beta strands \$1.83 are included in the structure of the scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to target the complex to tumour cells. For example, one surface of the scaffold contains the scaffold protein may be used to target the complex to tumour cells. Another surface may be bound to a protein which binds to a tumour antigen. The scaffore the scaffold protein may be used to target chemotherapeutic agents to especific cells. It may also be used in charged the changues, and to stabilize antigens used as vaccines. Sequences AAY40680-Y40703 are functionally equivalent derivatives of the

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75.5%; Score 74; DB 20; Length 16; 87.5%; Pred. No. 1.1e-05; ive 1; Mismatches 1; Indels
                       Best Local Similarity 87.5
Matches 14; Conservative
                                                                                       3 RLKSDNYATHYAESVK 18
  Query Match
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2 IRSKSDNYATYYANSVK 18

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Gaps

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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (I) their native structure; or (II) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. Pylori, H. hepaticus, the rapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequed to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
                                                                                                                                                                                                                                          Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heavy chain; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                       H. pylori 26 kDa protein-binding antibody heavy chain CDR2 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 70; DB 21; Length 19; 82.4%; Pred. No. 6.5e-05; ive 1; Mismatches 2; Indels
                                                                                            AAB10002 standard; Protein; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 21; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-0120517.
98EP-0120687.
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                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 82.4 es 14; Conservative
 1 RLNSDNFATHYAESVK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365747/31.
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                                                                                                                                                                                                                                                                                                                                                     WO200026671-A1.
                                                                                                                                                                                                                                                                                                                   Unidentified.
                                                                                                                                                                   01-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ringeis A;
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                                                                                                                                AAB10002;
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Mus musculus.
                                                                                    11-APR-2002
                                                                                                                                                                Hancock WW;
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                                                                                                                                                                                                                                                                                                                                                                                          (CDR2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; graft rejection; CC chemokine receptor 2 antagonist; CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse mab 1D9 antibody heavy chain complementarity determining region 2.
                                                                                                                                                                                                                                                                                                                                                               An antigen/antibody specificity exchanger comprises an antibody-derived amino acid sequence (A) which specifically binds to a particular antigen, linked to an amino acid sequence (C) to which example of a type (A) sequence; it is the CDR2 sequence of the heavy chain of monoclonal antibody C1.5. Preferred type (C) sequences are the antibody binding regions from viruses or other pathogens. The specificity exchanger can redirect antibodies already present in a patient and raised against a particular antigen, to fight a different antigen. For example, it was shown that anti-poliovirus antibodies could be redirected to fight HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                            Tailor-made, antigen/antibody specificity exchanger; HIV infection; MAb C1-5; heavy chain; complementarity determining region; human immunodeficiency virus; variable loop 3 domain; redirecting.
                                                                                                                                                                                                                                                                                                         Antigen-antibody specificity exchanger - used in a method to redirect a patient's antibodies against polio:virus to fight HIV infection in the patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 16; Length 19;
Pred. No. 0.00014;
3; Mismatches 2; Indels
                                                                                          CDRH2 of monoclonal antibody C1-5.
                                  AAR84529 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 34; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%;
                                                                                                                                                                                                             95WO-SE00468
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                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                        WPI; 1995-393040/50.
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Best Local Similarity
                                                                                                                                                                                                                                                 (FERR ) FERRING AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AA;
                                                                        06-JUN-1996
                                                                                                                                                                                                                              28-APR-1994;
                                                                                                                                                                                                            27-APR-1995;
                                                                                                                                                                     WO9529938-A1
                                                                                                                                                                                                                                                                     Saellberg M;
                                                                                                                                                                                         09-NOV-1995.
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                                                                                                                                                    Synthetic
                                                     AAR84529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                RESULT 6
                          AAR84529
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The invention comprises a method of inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft. The method involves administering an antagonist of CC chemokine receptor 2 (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may be an anti-CCR2 antibody (i.e. containing light and heavy chain complementarity determining regions from various non-human origins). CCR2 is known to be involved in the rejection of transplanted grafts. The method of the invention is useful for inhibiting graft rejection particularly allografts such as kidney, liver, lung, heart-lung, particularly allografts such as kidney, liver, lung, heart-lung, phancreas, bowel and heart. The method of the invention is also useful for inhibiting graft versus host disease and for inhibiting chronic rejection of a transplanted graft. The present amino acid sequence represents a mouse mAb 1D9 antibody heavy chain complementarity determining region 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody, MAb, lipoteichoic acid; gram positive, bacteria, immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
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/note= "complementarity determining region (CDR)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft, involves administering a CCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
lung transplant; heart-lung transplant; pancreas transplant; bowel transplant; heart transplant; graft versus host disease; chronic graft rejection; antibody heavy chain; mAb 1D9; CDR2; complementarity determining region 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 19; 0.00045; ches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 2
Pred. No. 0.000
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-2001; 2001US-0835087.
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70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-2000; 2000US-0549448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IRLKSDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IRTKNNNYATYYADSVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.3
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-351265/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 AA;
                                                                                                                                                                                                                                                          US2002042370-A1
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WO9857994-A2

23-DEC-1998

16-JUN-1998; 16-JUN-1997;

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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdab fragments) derived from liama antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it antigen-binding fragments having high affinity to almost any predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies by immunisation and allows the llama heavy chain domain fragments of the invention.
                                                                                                                                       New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-CDR-2 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new anti-idiotype antibody against a human anticancer monoconal antibody is claimed. This antibody contains in its heavy chain 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 23; Length 17;
Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74934 standard; peptide; 19 AA.
                                                                                                                                                                                                                                       Claim 16; Page 32; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2; 28pp; Japanese.
(CANA ) NAT RES COUNCIL CANADA.
                                             Dubuc G, Narang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0272950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-182987/24.
                                                                                          WPI; 2002-083093/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP07101999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-1996
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                                             Tanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR74934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria! They can also sequences AAW94735-39 represent heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llama; phage display library; variable heavy domain fragment; VHH; VH; sdAb fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                 New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 20; Length 19;
Pred. No. 0.00065;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Llama CDR2 region variable heavy chain fragment #32.
                                                                                                                                                                                       (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                  Stinson JL, Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU82539 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Fig 12; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-207234P.
                                                                                        98WO-US12402.
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                                                                                                                                                                                                                                  Fischer GW, Schuman RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       guanicoe glama.
                                                                                                                                                                                                                                                                                  WPI; 1999-095329/08.
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                                                                                                                                                                                                                                                                                                        N-PSDB; AAX05581
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Sequence Query Match 29-NOV-2001

Lama

AAU82539;

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Gaps

19 AA;

Sequence

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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynuclectides cenceding different immunoglobulin binding protein (198P) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an 198P that confines to a ligand, and transformed plant cells are selected, and preparing an 198P array in plant cells. At least one peptide sequence has confined and transformed plant cells. At least one peptide sequence at least 75* sequence identity to a framework region (FR) of a native confines, 196, 199, 199, 198, 197, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (GHBP) array in eukaryotic cells (e.g. Aprobacterium tumefaciens or maize) or other eukaryotic cells (e.g. Aprobacterium tumefaciens or maize) conther eukaryotic cells (e.g. insect cells or mammalian cells). The GHBP is useful for discovery of e.g. screening assays of 19BPs having confined characteristics. The present sequence is a mammalian cells. The invention.
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complemetarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932-R794931), this is also true of the light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3 (AAR74954). The antibody and DNA encoding it are useful in pharmacological, medical and blochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin, antibody; light chain; heavy chain; CDR; FR; conplementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                       16; Length 19;
                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                       50.0%; Score 49; DB 16
55.6%; Pred. No. 0.21;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               AAU70371 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000; 2000US-0563222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human heavy chain III CDR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2001; 2001WO-US14349.
                                                                                                                                                                                                                                                                       2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                              2 IRNKANYYTTEYSASVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002 (first entry)
                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                             Query Match
Best Local Similarity
Marches 10; Conserv
                                                                                                                                                    19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU70371;
                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides cancing different immunoglobulin binding protein (198P) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transferded cells, to generate an 198P that binds to a ligand, and transformed plant cells are selected, and preparing an igpP array in plant cells. At least one peptide sequence identity to a framework region (FR) of a native 198, 196, 198, 190, 198, 197, kappa or lambda immunoglobulin molecule. The machod is useful for preparing an immunoglobulin binding protein carray, preferably plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of 198Ps having desired characteristics. The present sequence is a mammalian cile or immunoglobulin derived peptide that may be incorporated into an 198P of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                               Gaps
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                               ö
                                                                                                                                                                                                                                                                                                           Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgB; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 23; Length 19;
Pred. No. 0.31;
4; Mismatches 4; Indels
DB 23; Length 19;
                               5
                               4; Mismatches
Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 15; 129pp; English.
                                                                                                                                                                                AAU70380 standard; Peptide; 19 AA.
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Similarity 52.9%;
9; Conservative '
50.0%;
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                                                                                                                                                                                                                                                                               Mouse heavy chain III CDR 2.
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                                                                                                                                                                                                                                                (first entry)
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                                Conservative
                                                                 5 KSDNYATHYAESVKG 19
                                                                                 |:| :|:||:|||
5 KTDGGSTXYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-055482/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
 Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                 RESULT 12
AAU70380
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The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity determining region 2; Campath-1; Campath-1H; antibody; lymphoma; CD52 antigen; loop 2; immunological tolerance; minimal mutant; antibody therapy; antiglobulin response; heavy chain; CDR.
                                                                                                                                                                                                                                                                               Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= K7D
/note= "wild type Lys substituted with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%; Score 46; DB 21; Length 17; 52.9%; Pred. No. 0.59; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant 3 of the CDR2 region of the Campath-1H heavy chain.
                                                                                                                                                                                                             Sablon E;
                                                                                                                                                                                                           Hoodenboom H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 14; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23392 standard; peptide; 19 AA.
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                                                                                                     99WO-EP02283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 52.9
Les 9; Conservative
                                                                                                                                                                           (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                           Desmet J, Hufton S,
                                                                                                                                                                                                                                               WPI; 2000-665002/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 AA;
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                                 WO200060070-A1.
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                                                                                                     01-APR-1999;
                                                                                                                                       01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1997
                                                                   12-OCT-2000
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                        fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new anti-idiotype antibody against a human anticancer monoconal antibody is claimed. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (ARR14929-R74911), CDR2 (AAR74932-R794935) and CDR3 (AAR74936-R74939), this is also true of the light chain which has its own CDR1 (AAR74944-R74946 and AAR8774), CDR2 (AAR74947-R74949) and CDR3 (AAR74956-R74954). The antibody and DNA encoding it are useful in pharmacological, medical and biochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               H-CDR-2 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                 Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scaffold protein SCA A3 peptide SEQ ID NO: 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB30034 standard; Peptide; 17 AA.
                                                                                                                                       AAR74933 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 2; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93JP-0272950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IRNKANLYTTDYSASVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                   | |:::| | |: ||||
RNKANDYTTEYSASVKG 19
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                RLKSDNYATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-182987/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA;
                                                                                                                                                                                                                                                                                                                                                                        JP07101999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1993;
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                                                                                                                                                                                                           19-JAN-1996
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                                                                                                                                                                       AAR74933;
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Matches

RESULT 14 AAB30034

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Gaps

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Peptides AAW23390-95 represent "minimal" mutant sequences of the complementarity determining (CDR) region 2 of the humanised antibody Campath-11. Campath-111 heavy chain sequence encodes human protein at all positions, except the 3 CDR regions. Campath-1 antibodies have been used to induce remissions in lymphoma and leukemia patients and for the treatment of rheumatoid arthritis and vasculitis. The target and for the treatment of rheumatoid arthritis and vasculitis. The target and for DS2, which is a GDI-anchord cell-surface glycoprotein of lymphocytes and monocytes. Loop 2, represented by residues 4-9 of the present sequence, is important for binding to CD52. Mutations were made within this region so as to abolish binding of the antibody to CD52, which reduces affinity for the antigen, and induces immunological tolerance. The present mutant contains a single charge difference from Lys to Asp. The positive charge of Lys is thought to interact with the not this single mutation may destroy antigen binding. Antibody therapy is often limited by an anti-antibody (antiglobulin) response preventing retreatment with the antibody. The minimal mutants or preventing retreatment with the antibody. The minimal mutants or patients may be used to induce tolerance to the therapeutic antibody in patients. They can also be used in the manufacture of medicines for induction of tolerance.
                                                                                                                      Modified therapeutic antibody having reduced affinity for its antigen - can induce immunological tolerance, e.g. to Campath-1 monoclonal antibodies used in antibody therapy of lymphoma and
                Tone M, Waldmann H, Walsh L;
                                                                                                                                                                                                                                                              Claim 12; Fig 1; 43pp; English.
                        Gilliland LK,
                                                                       WPI; 1997-435093/40.
                        Frewin MR,
                                                                                                                                                                                                               leukaemia
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Score 45; DB 18; Length 19; Pred. No. 0.98; 1; Mismatches 7; Indels Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative 19 AA; Sequence

2 IRLKSDNYATHYAESVKG 19

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0; Gaps

2 IRDKADGYTTEYNPSVLG 19 ò 셤 Search completed: April 22, 2003, 13:48:26 Job time : 74 secs

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

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STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURBNT APPLICATION DATE: 19-Apr-2001
CLASSIFICATION: -CURRONS-
PRIOR APPLICATION: -CURRONS-
PRIOR APPLICATION: -CURRONS-
PRIOR APPLICATION: -CURRONS-
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: 08/737,085
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
EXCHANGER
        US-09-968-561A-38

US-09-968-561A-68

US-09-968-561A-90

US-09-968-561A-92

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-140

US-09-968-561A-140

US-09-968-561A-140

US-09-968-561A-140

US-09-968-561A-188

US-09-968-561A-189

US-09-968-561A-189

US-09-968-561A-189

US-09-968-561A-212

US-09-968-561A-218

US-09-968-561A-218
                                                                                                                                                                                                                                                                    -09-968-561A-296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09839666
Patent No. US20020025513A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
US-09-839-666-4
RESULT 1
Sequence 290, App
Sequence 164, App
Sequence 85, Appl
Sequence 56, Appl
Sequence 37, Appl
Sequence 6, Appl
Sequence 18, Appli
Sequence 200, App
Sequence 200, App
Sequence 200, App
Sequence 115, Appli
Sequence 115, Appli
Sequence 115, Appli
Sequence 115, Appli
Sequence 6, Appli
Sequence 115, Appli
Sequence 115, Appli
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Sequence 18, Appl
Sequence 98, Appl
Sequence 60, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             April 22, 2003, 13:49:38 ; Search time 41 Seconds (without alignments) 37.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
        GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-192-854.60

US-09-192-854.164

US-09-125-460A-14

US-09-125-460A-14

US-09-130-857-85

US-09-192-854-37

US-09-192-854-37

US-09-192-854-37

US-09-88-51A-20

US-09-968-561A-20

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US-09-192-854-115
US-09-125-460A-6
US-09-968-561A-14
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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US-09-835-087-18
                                                                                                                                                                                                                  301932 segs, 80129803 residues
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                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                                                                                                     1 BIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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98
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Match Length
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Perfect score:
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Maximum DB
                                                        protein
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Sequence 290, Application US/09968561A

Sequence 200, Application US/09968561A

Sequence 200, Application US/09968561A

GENERAL INFORMATION:

APPLICANT: TOMILISON: Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

FILE REFERENCE: 8039/1073B

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT APPLICATION NUMBER: US 60/065,248

FRIOR PELING DATE: 1997-11-21

PRIOR PILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR PELING DATE: 1997-11-21

PRIOR PILING DATE: 1998-10-20

PRIOR PILING DATE: 1998-10-20

PRIOR PILING DATE: 1998-10-20

PRIOR SED ID NOS: 350

SOFTWARE: Patentin version 3.1

LEMBER OF SEQ ID NOS: 350

SEQ ID NO 290
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; Batent No. US20020068276A1
; GABERAL INFORMATION:
    APPLICANT: Winter, Greg
    APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/22916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT APPLICATION NUMBER: 60/066,729
; BARLIER APPLICATION NUMBER: 60/066,729
; BARLIER PILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PAT
    CRANISM: Homo sapiens
US-09-192-854-60
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Pred. No. 0.22;
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                                                                                                                     Score 48; DB 9; Length 17;
Pred. No. 0.22;
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Pred. No. 0.45;
                                                                                                                                                                                     3; Mismatches
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                                                                                                                     49.0%;
52.9%;
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1 RIPARGTVTHYADSVKG 17
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1 RIPARGTVTHYADSVKG 17
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                                                                                                                                                   Best Local Similarity 52.9
Matches 9, Conservative
                                    ; ORGANISM: Homo sapiens
US-09-968-561A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                           Query Match
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US-09-968-561A-98
IS-09-968-561A-98
Sequence 98, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
ITILE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 3039/1073B
CURRENT PAPLICATION NUMBER: US/09/968,561A
FRIOR FILING DATE: 1997-10-01
FRIOR FILING DATE: 1997-11-03
FRIOR FILING DATE: 1997-11-13
FRIOR PLING DATE: 1997-11-21
FRIOR FILING DATE: 1997-11-21
FRIOR FILING DATE: 1997-11-20
FRIOR FILING DATE: 1997-11-20
FRIOR PLICATION NUMBER: US 60/066,729
FRIOR PLICATION NUMBER: US 60/066,729
FRIOR FILING DATE: 1997-11-20
FRIOR PLICATION NUMBER: US 60/066,729
FRIOR PLICATION NUMBER: US 60/061,729
FRIOR FILING DATE: 1997-11-21
FRIOR PLICATION NUMBER: US 60/511,939
FRIOR FILING DATE: 1990-10-20
FRIOR FILING DATE: 1990-1
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; OTHER INFORMATION: CDR2 of murine mAb 1D9 heavy chain variable region
US-09-835-087-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-09-835-087-18
Sequence 18, Application US/09835087
Sequence 18, Application US/09835087
Settle No. US20020042370A1
GENERAL INFORMATION:
APPLICANT: WAYNEW HELD OF THE SETTLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 1855.2009-003
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/649,448
PRIOR APPLICATION NUMBER: 09/649,448
PRIOR APPLICATION NUMBER: 09/649,448
PRIOR PLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 18
LENGTH: 19
LENGTH: 19
                                                                                                                                                   Score 68; DB 10; Length 19;
Pred. No. 0.00017;
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Pred. No. 0.00051;
                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-666-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.3%;
                                                                                                                                             Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
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Best Local Similarity 70.6
Matches 12; Conservative
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US-09-968-561A-56
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                                        -09-730-857-85
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                                                                                                                                                                                                                                             APPLICANT: Winter, Greg
APPLICANT: Winter, Greg
APPLICANT: Conlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: 08/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER FILING DATE: 1998-11-17
EARLIER FILING DATE: 1997-11-21
SOFTWARE: PATENTIN NOS: 212
SOFTWARE: PATENTIN VOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 45; DB 10; Length 19; 55.6%; Pred. No. 0.73; tive 1; Mismatches 7; Indels
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  Indels
  4;
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Pred. No. 0.45;
1; Mismatches
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APPLICANT: TONE, MASAHIDE
APPLICANT: TONE, MASAHIDE
APPLICANT: TONE, MASAHIDE
APPLICANT: WALSH, LOUISE
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: PP/NT/2794 US
CURRENT APPLICATION NUMBER: US/09/125,460A
CURRENT FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: PCT/GB97/00472
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: GB 9603507.6
1; Mismatches
                                                                                                                                                                                   Sequence 164, Application US/09192854 Patent No. US20020068276A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09125460A
Patent No. US20020046578A1
GENERAL INFORMATION:
APPLICANT: WALDMANN, Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IRLKSDNYATHYAESVKG 19
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Best Local Similarity 64.3
Matches 9; Conservative
Conservative
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                                          SDNYATHYAESVKG 19
                                                                                SSGYGTGYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-192-854-164
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LENGTH: 19
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Gequence 56, Application US/09968561A

Patent No. US2020164642A1

GENERAL INFORMATION:
APPLICANT: Tomilinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILE TOMILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR PLING DATE: 1997-10-20
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                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Machington
STATE: DC
Sequence 85, Application US/09730857

Patent No. US20020082396A1

GENERAL INFORMATION:

APPLICANT: Mateushima, Kouji

Mateushima, Yoshihiro

Yamada, Yoshiki

Sato, Koh

Tsuchiya, Masayuki

Yamazaki, Tateumi

TITLE OF INVENTION: Reshaped Human Antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-Dec-2000
CLASSIFICATION: cUtknown>
PRIOR APPLICATION DATA: cUtknown>
APPLICATION NUMBER: 09/416,557
FILING DATE: 1999-10-12
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

CONDUTER: 2006-1888

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/730,857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IRLKSDNYATHYAESVKG 19
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Sequence 8, Application US/09968561A;
Sequence 8, Application US/09968561A;
Patent No. US20020164642A1
GENERAL INFORMATION:
HAPPLICANT: Tomlingon, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands;
TITLE REFERENCE: 8039/10/33B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 1997-10-01
FRIOR APPLICATION NUMBER: US 60/065,248
FRIOR FILING DATE: 1997-11-13
FRIOR FILING DATE: 1997-11-13
FRIOR FILING DATE: 1997-11-13
FRIOR FILING DATE: 1997-11-20
FRIOR FILING DATE: 1998-10-20
FRIOR FILING DATE: 1998-10-20
FRIOR FILING DATE: 1998-10-20
FRIOR FILING DATE: 1998-10-20
FRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFFWARE: PATENTIN VERSION 3.1
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US-09-798-058-6
US-09-98-058-6
US-09-98-058-6
US-09-98-058-6
US-09-98-058-6
US-09-058-6
US-02-0200098523A1
US-02-02-02
US-02-02-02-02
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                                                                                                            Query Match 43.9%; Score 43; DB 10; Length 17; Best Local Similarity 47.1%; Pred. No. 1.3; Matches 8; Conservative 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                         1 RISGNSGSTFYADSVKG 17
                                                                                                                                                                                                                                                  3 RLKSDNYATHYAESVKG 19
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Best Local Similarity 61.5
Matches 8; Conservative
              ; ORGANISM: Homo sapiens US-09-828-708-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-09-798-058-6
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LENGTH: 17
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Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Birton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particily TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particily TITLE OF INVENTION: AUTOIMMUNE disease
FILE REFERENCE: 1361.005US1
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
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Fatent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Wincer, Greg
FAPPLICANT: Wincer, Greg
FILE REFERENCE: 3789/72916
CURRENT FAPLICATION NUMBER: US/09/192,854
CURRENT FILE OF INVENTION NUMBER: US/09/192,854
CURRENT FILE OF 199-11-17
EARLIER APPLICATION NUMBER: 60/066,729
FARLIER FILING DATE: 199-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.3;
4; Mismatches 5; Indels
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PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 56
LENGTH: 17
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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1 RITPAGHRTYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-56
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US-09-192-854-37
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LENGTH: 17
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                                                                                       Length 17;
                                                                                       Score 41; DB 9;
Pred. No. 2.8;
1; Mismatches
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                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
      ; ORGANISM: Homo sapiens
US-09-968-561A-206
                                                                                                                                                                                                       10 ATHYAESVKG 19
                                                                                                                                                                                                                                     8 ATRYADSVKG 17
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Sequence 2004, Application US/09968561A __
Sequence 2004, Application US/09968561A __
Sequence 2000, Application US/09968561A __
Sequence 2000, Application US/09968561A __
SEMERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
TILE REPERBENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT APPLICATION NUMBER: US 001-10-01
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR PILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PERIOR PERI
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Pred. No. 2.8;
1; Mismatches 1; Indels
Query Match
41.8%; Score 41; DB 9; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.8;
Matches 8; Conservative 3; Mismatches 3; Indels
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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4 SEGWPTIYADSVKG 17
                                                                                                               6 SDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-09-968-561A-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ATHYAESVKG 19
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8 ATRYADSVKG 17
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US-09-968-561A-206
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Sequence 86, Appl
Sequence 65, Appl
Sequence 65, Appl
Patent No. 5496552
Sequence 16, Appl
Patent No. 5169835
Sequence 81, Appl
Sequence 83, Appl
Sequence 80, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 61, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
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Sequence (
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Pred. No. 8.6e-05;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08737085A
Patent No. 586922
GENERAL INFORMATION
APPLICANT: SALIBERG, MATTI
TITLE OF INVENTION: EXCHANGER
INTER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZOUNTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY-AGENT INPORMATION:
WANTE: COCCOL. DESC.
US-08-285-936-54
US-08-847-860-54
US-08-104-744-86
US-08-704-744-86
US-08-290-7938-65
5496552-4
US-09-406-532-16
US-09-406-532-16
US-09-406-532-16
US-08-208-886C-81
US-08-208-886C-81
US-08-704-744-90
US-08-704-744-91
US-08-36-953A-29
US-08-36-953A-21
US-08-36-953A-21
US-08-36-953A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 236697

INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.2
Matches 13; Conservative
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US-08-737-085A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
  RESULT 1
US-08-737-085A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       April 22, 2003, 13:47:08 ; Search time 14 Seconds (without alignments) 39.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4,
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: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-737-085A-4
US-09-246-258-4
US-09-246-258-4
US-09-839-666-4
US-09-839-666-4
US-08-976-586-78
US-08-976-288-78
US-08-976-288-78
US-08-18-970B-5
US-08-18-970B-5
US-08-416-557-85
US-08-416-557-85
US-08-452-724A-41
US-08-452-724A-41
US-08-452-724B-41
US-08-486-434-33
US-08-480-434-33
US-08-480-434-33
US-08-480-53-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
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US-08-053-451B-34
US-09-170-769A-11
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08-244-626-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                       1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                US-09-674-716B-11
98
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                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 19
                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Maximum DB
                                                                                                                                                                                                                                                                                                            Sequence:
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                                                                                                                                                              Run on:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FASESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Mar-2000
PRION APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
ATTORNEY/ABGNI INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REGISTRATION NUMBER: 38,475
RETERPAK: 212-527-7659
TELECHONE: 212-527-7659
TELECHONE: 212-527-7659
TELERY: 216-753-6237
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACTERSICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
CITY: New York
CUMPR: USA
ZIP: 10022
COMPUTR: USA
ZIP: 10022
COMPUTR: EDSA
MEDIUM TYPE: Diskette
COMPUTR: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESCE FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-APL-2001
CLASSIFICATION: AUMROWN:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/737,085
FILING DATE: CUMROWN:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09839666
Patent No. 6469143
GENERAL INPOMATION:
APPLICANT: SALLBERG, MATTI
TIPLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; I
8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-532-106-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS ARBY PC
ADDRESSEE: DARBY & DARBY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
  ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-839-666-4
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                                                                                                       Sequence 4, Application US/09246258
; Patent No. 6040137
; GENERAL INFORMATION:
    APPLICANT: SALIBERG, MATTI
    TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
    TITLE OF INVENTION: EXCHANGER
    NUMBER OF SEQUENCES: 23
    CORRESPONDENCE ADDRESS:
    STREET: BOS Third Avenue
    STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09532106
Patent No. 6245895
GENERAL INFORMATION:
APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 3; I
Pred. No. 8.6e-05;
3; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green. Reza
REGISTRATION NUMBER: 38,475
REPERENCE/DOCKET NUMBER: 3846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IRLKSDNYATHYAESVKG 19
2 VRSKSFNYATYYADSVKG 19
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212-753-6237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-09-246-258-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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Gaps

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RESULT 7
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Sequence 78, Application US/0797696C

Retent No. 5792852

GENERAL INFORMATION:

APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Pederson Dr., Jerry A.

APPLICANT: Pederson Dr., Beduardo A.

TITLE OF INVENTION: Eduardo A.

TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination

TITLE OF INVENTION: and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSER: PRETTY, SCHROEDER & POPLAWSKI

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                69.4%; Score 68; DB 4; Length 19; ilarity 72.2%; Pred. No. 8.6e-05; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: ....
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM FC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMZEI Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (510) 748-6688
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
TELEFAX: 212-753-6237
TELEX: 236697
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIRLKSDNYATHYAESVKG 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Best Local Similarity
Matches 13; Conserv
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UB-08-129-308-78

UB-08-129-308-78

Patent No. 5604187

Patent No.
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US-60-118-970B-5

1 Sequence 5, Application US/08318970B

1 Patent No. 5599573

2 REMERAL INFORMATION:

APPLICANT: Hideaki HAGIWARA, et al.

TITLE OF INVENTION: ANNIA ALIDEADES AGAINET ANTI-CANCER HUMAN MONOCLONAL

TITLE OF INVENTION: ANNIADOIES AGAINET ANTI-CANCER HUMAN MONOCLONAL

TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

INVERSPONDENCE ADDRESS:

ADDRESSE: Law Office of Sherman and Shalloway

STREET: 413 N. Washington Street

CITY: Alexandria

STATE: Virginia

CONPITER: Dell System 210, Intel 80 285 Microprocessor

CONPITER: Word Perfect, Version 5.1

CONPITER: Word Perfect, Version 5.1

CURRENT APPLICATION NUMBER: 18, 26, 1994

CLASSIFCATION NUMBER: 26, 588

REGISTATION NUMBER: 26, 588

REPERENCE/DOCKET NUMBER: 8, 25, 318

TELLOROMYLICATION NUMBER: 26, 588

REFERENCE/DOCKET NUMBER: 8, 25, 318

TELLOROMYLICATION NUMBER: 26, 588

REFERENCE/DOCKET NUMBER: 8, 25, 318

TELLOROMYLICATION NUMBER: 26, 588

REFERENCE/DOCKET NUMBER: 8, 25, 318

TELLOROMYLICATION NUMBER: 9, 318

TELLOROMYLICATION NUMBER: 9, 318

TODOLOGY: Himear

TODOLOGY: Himear

TODOLOGY: Himear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

50.0%; Score 49; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 5; Indels
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; OTHER INFORMATION: hypervariable region
US-08-318-970B-5
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: H-CDR2-3
OTHER INFORMATION: hypervariable region
US-08-318-970B-6
                      REFERENCE/DOCKET NUMBER: S-23.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 845-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
REGISTRATION NUMBER: 26,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IRNKANYYTTEYSASVKG 19
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                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-318-970B-5
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Sequence 6, Application US/08318970B

Patent No. 5589573

GENERAL INFORMATION:

APPLICANT: Hideaki HAGIWARA, et al.

TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC

TITLE OF INVENTION: AND DAM BASE SEQUENCES ENCODING THOSE SEQUENCES

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Office of Sherman and Shalloway

STREET: Ala N. Washington Street

CITY: Alexandria

STATE: Virginia

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: Dell System 210; Intel 80 285 Microprocessor

COMPUTER: Dell System 210; Intel 80 285 Microprocessor

OPERATING SYSTEM: Mord Derfect, Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/318,970B

FILING DATE: October 6, 1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Richard A. Steinberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.3%; Score 66; DB 4; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00018;
Matches 13; Conservative 4; Mismatches 2; Indels
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPOPY disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORPOTES: IBM PC compatible
CORPOTES: IBM PC compatible
CORPOTES: SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION NUMBER: 08/129,930
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 489-4210
             444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEKAN.
TELEK: n.a.
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
             STREET: 444 South F
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-976-288A-78
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JUS-264-02-22, Application US/08264093

Patent No. 5639863

Patent No. 5639863

JAPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESONDENCE ADDRESS: 36
CORRESONDENCE ADDRESS: ADDRESS: Ridout & Maybee STREET: 2300 Richmond-Adelaide Centre STREET: 101 Richmond Street West CITY: Toronto CITY: Toronto COUNTRY: Canada
STREET: 101 Richmond Street West CITY: Toronto COUNTRY: Canada
ZIP: MSH 2J7
COMPUTER: BADABLE FORM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
APPLICANT: Yamazaki, Tateumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: 2000 CITY: USA
ZITE: 1050
COUNTRY: USA
ZITE: 1050
COUNTRY: USA
ZITE: 1050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESCE for Windows Version 2.0
SOFTWARE: FESTESCE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,557
FILING DATE: 12-October-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,783
FILING DATE: 7-March-1997
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTATION NUMBER: 29,959
REGISTATION NUMBER: 29,959
REGISTATION INFORMATION:
TELEFONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
45.9%; Score 45; DB 4;
Best Local Similarity 50.0%; Pred. No. 0.45;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-416-557-85
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Pred. No. 0.45;
3; Mismatches 6; Indels
                                                                                                                                 Sequence 65, Application US/08765783A

Sequence 65, Application US/08765783A

Patent No. 5994524

RENERAL INFORMATION:

APPLICANT: Matsushima, Kouji

APPLICANT: Yamada, Yoshiki

APPLICANT: Yamada, Yoshiki

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Tsuchiya, Masayuki

TTTLE OF INVENTION: Interleukin-8

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STREET: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UGA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILIAS DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35029-20001.20
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Patent No. 6245894
GENERAL INFORMATION:
APPLICANT: Matsumbto, Yoshihiro
APPLICANT: Wandama, Yoshihiro
APPLICANT: Sato, Koh
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAISANIGE, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IRLKSDNYATHYAESVKG 19
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                                                 2 IRNKANLYTTDYSASVKG 19
            2 IRLKSDNYATHYAESVKG 19
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Best Local Similarity 50.0°
Matches 9; Conservative
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US-09-416-557-85
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Gaps

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Gaps
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Patent No. 5866124
Fatent No. 5866124
Fatent No. 5866124man
Patent No. 5866124man
APPLICANT: Hardman, No. 5866124man
APPLICANT: Hardman, No. 5866124man
APPLICANT: Huschke, Gerd
APPLICANT: Murray, Brendan
TITLE OF INVENTION: Genetically engineered antibodies
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866124artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: NJ
COUNTRY: USA
COMPUTER: NJ
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                    Score 39; DB 2; Length 14;
Pred. No. 3;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: DE 92810188.0
FILING DATE: 17-MAR-1992
ATTORNEY/AGENT INFORMATION:
ATMARE: Henry P. No. 5866124ak
REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION
TELEPHONE: 908-277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.8%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 amino acida
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Best Local Similarity 43.6
Matches 7; Conservative
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                                                                                                            Query Match 39.8
Best Local Similarity 53.8
Matches 7; Conservative
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HYPOTHETICAL: 1
                                        US-08-452-724A-41
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US-08-053-171-31
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US-08-650-262-14
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US-08-452-724A-41
Sequence 41, Application US/08452724A
Sequence 41, Application US/08452724A
FERENT NO. 5830650
FENERAL INFORMATION:
APPLICANT: Crea, Roberto
FILLE OF INVENTION: Walk-Through Mutagenesis
MUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMBUTER PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.9%; Score 44; DB 1; Length 17; 50.0%; Pred. No. 0.57;
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FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:

NAME: Lake, James R.

REGISTRATION NUMBER: 31081

REFERENCE/DOCKET NUMBER: NOVOP/106A/7551

TELECOMUNICATION INFORMATION:

TELEPAX: (416) 362-0823

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acid

STRANDEDNESS: not applicable

TYPE: amino acid

STRANDEDNESS: not applicable

JOPOGLOGY: linear

US-08-264-093-22

#44.9%; Score 44; DB 1;
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TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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us-09-674-716b-11.closed.rai

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CORRESPONDENCE ADDRESS:
ADDRESSES:
Townsend and Townsend Khourie and Crew
STREET:
Talo ALG.
STREET:
STATE:
CALIfornia
COMPURE:
CO
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Search completed: April 22, 2003, 13:50:14 Job time : 15 secs

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Run on:

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APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabar Doron
APPLICANT: Shabar Doron
APPLICANT: Shabar, Doron
APPLICANT: Rader, Christoph
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PROBUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF0011S
CURRENT APPLICATION NUMBER: US/09/318,661
CURRENT APPLICATION NOWBER: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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11. /cgn2_6/ptodate1/liaa/5A_COMB.pep:*
12. /cgn2_6/ptodate1/liaa/5B_COMB.pep:*
3. /cgn2_6/ptodate1/liaa/6A_COMB.pep:*
43. /cgn2_6/ptodate1/liaa/6B_COMB.pep:*
55. /cgn2_6/ptodate1/liaa/PCTUS_COMB.pep:*
6. /cgn2_6/ptodate1/liaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-318-661-2

US-08-466-272A-1

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US-09-130-783-1

US-08-483-749A-2

US-08-483-749A-2

US-08-767-128-28

US-08-767-128-26

US-08-767-128-26

US-08-192-102-5

US-08-192-861A-5

US-08-192-861A-5

US-08-192-861A-5

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US-08-192-861A-5

US-08-192-66-45

US-08-661-432-2

US-08-661-445-2

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Result

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24, Appl
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US-08-129-930B-78
US-08-976-288A-78
US-08-129-930B-73
US-08-129-930B-13
US-08-129-930B-13
US-08-442-542-14
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US-08-765-469-12
US-08-765-469-12
US-08-765-469-18
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US-08-525-539A-33
US-07-942-245-21
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## ALIGNMENTS

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Sequence 4, Application US/09318661
; Sequence 4, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
    APPLICANT: Shabat, Doron
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: Larner, Richard A.
    TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; TURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2:1
; SEQ ID NO 4
; LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: residue sequence of catalytic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 98; DB 4; Length 285; Best Local Similarity 100.0%; Pred. No. 2.4e-08; Matches 19; Conservative 0; Mismatches 0; Indels
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US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6268488
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bosslet, Klaus
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                     Length 298;
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                                                             Score 95; DB 4; Length 230
Pred, No. 7.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 2005-3315

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,661
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
PROOR APPLICATION: 530
PROOR APPLICATION: 530
PROOR APPLICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: FORMAN, DAVIG S.
REGISTRATION NUMBER: 35,694
REFERENCE/DOCKET NUMBER: 35,694
REFERENCE/DOCKET NUMBER: 35,694
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBEHOUS: 202-408-4000
                                                                            Query Match 96.9%; Score 95; DB Best Local Similarity 94.7%; Pred. No. 7.8e Matches 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08468661
; Patent No. 5639621
; GENERAL INFORMATION:
                                                                                                                                                                                  205 EIRLRSDNYATHYAESVKG 223
                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
TYPE: PRT CORGANISM: Mus musculus US-09-318-661-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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RESULT 4

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Sequence 1, Application US/09130783

Sequence 1, Application US/09130783

Sequence 1, Application US/09130783

GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Pfleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for TITLE OF INVENTION: Preparation Thereof and the Use Thereof NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 3; Length 115;
Pred. No. 5.7e-08;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                                                                       94.9%; Score 93; DB 2; Length 115
94.7%; Pred. No. 5.7e-08;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
CONMIRY: USA
ZID: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/130,783
FILING DATE:
CLASSIFICATION NUMBER: US/09/130,783
FILING DATE:
PLING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                              05552-1227-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C.
                                                       REFERENCE/DOCKET NUMBER: 0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEFAX: 202-408-400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Forman, David S. REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                               REGISTRATION NUMBER: 33,694
                                                                                                                                                         TYPE: amino acids
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 115 amino acids
amino acid
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Best Local Similarity 94.79
Matches 18; Conservative
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                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-471-771-1
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US-09-130-783-1
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APPLICANT: Pfleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/471,771
FILING DATE: 06-UNDE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
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ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,857
                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BUGALSKY, LAWTENCE B.
REGISTRATION NUMBER: 35,086
REGISTRANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08471771
Patent No. 5837824 .
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-4408-4400 INFORMATION FOR SEQ 1D NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 115 amino acids
                                                  ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Forman, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 EIRLKSNNYATHYAESVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                             FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-478-857-1
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Sequence 2, Application US/08483749A

Patent No. 6054561

GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CANCER CONTINUE
STATES CANCER CONTINUE
STATES CANCER CONTINUE
STATES CANCER CANCE
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SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REGISTRATION NUMBER: 36,914
REGISTRATION NUMBER: 36,914
RETERRENCE/DOCKET NUMBER: 36,914
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONE: (510) 601-2585
INPORMATION PROPAGITICS:
SEQUENCE (GLARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acids
TATES amino acids
TATES THE APPLICATION OF ACIDS
TOTAL OF ACIDS OF ACIDS
TOTAL OF ACIDS 
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ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.9%;
50 EIRLKSNNYATHYAESVKG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
                                                                                                                                                                                         RESULT 9
US-08-483-749A-2
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                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: WILE, DWANE E.

APPLICANT: LOPEZ, OSVALDO

APPLICANT: MIRRAY, PETER

TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND

TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6111079west Center, 90 South Seventh St

CITY: Minneapolis

STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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94.9%; Score 93; DB 3; Length 120;
Best Lycal Similarity 94.7%; Pred. No. 6e-08;
Matches 18; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UN-1996
PRIOR APPLICATION DATA:
APPLICATION WIMBER: PCT/US96/09258
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA: 08/541,373
FILING DATE: 10-OCT-1995
ATTONEY/AGENT INFORMATION:
NAME: CALCE, Charles G.
REGISTATION NUMBER: 35,093
REFERENCE/DOCKT NUMBER: 35,093
REFERENCE/DOCKT NUMBER: 8448.49USF1
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 55402
ZIP: 55402
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                          RESULT 8
US-08-767-128-28
; Sequence 28, Application US/08767128
; Patent No. 6111079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids TYPE: amino acid strandedness: single
                                                                                     46 EIRLKSNNYATHYAESVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal ORIGINAL SOURCE: US-08-767-128-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                Gaps
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US-08-483-749A-10
US-08-483-749A-10

SQUENCE 10, Application US/08483749A

Patent No. 6054561

TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
ONRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
CONUTRY: USA
COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TRM PC COMDATIBLE
                                                .
0
Score 93; DB 3; Length 122;
Pred. No. 6.1e-08;
                                              0; Indels
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
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Gaps
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APPLICANT: Daddon, Peter E.
APPLICANT: Siegel, John
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
APPLICANT: MAINITON: ANTI-TNF ANTIBODIES
APPLICANT: MAINITON: ANTI-TNF ANTIBODIES
ANDRESSPONDENCE ADDRESS: 19
COMPRESS: Home ANTI-TNF ANTIBODIES
APPLICANTION: ANTI-TNF ANTIBODIES
APPLICANTION: ANTI-TNF ANTIBODIES
APPLICANTION: ANTI-TNF ANTIBODIES
APPLICANTION MAINITON: Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
STREET: Two Militia Drive
COMPUTER: Leathagen
STREET: Two Militia Drive
STREET: Two Militia Drive
APPLICANTON NUMBER: US/08/192,102
APPLICANTON NUMBER: US/08/192,093
FILING DATE: 04-FEB-1994
APPLICANTON NUMBER: US 08/010,406
FILING DATE: 11-SEP-1992
APPLICANTON NUMBER: US 07/943,852
FRILNG DATE: 11-SEP-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/943,652
FRILNG DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US 07/943,652
FRILNG DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US 07/943,652
FRILNG DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US 07/670,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 82.1%; Score 80.5; DB 3; Length 119; Best Local Similarity 89.5%; Pred. No. 6.2e-06; Matches 17; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-192-102-5; Sequence 5, Application US/08192102; Patent No. 5656272
                                                 REFERENCE/DOCKET NUMBER: 86
TBLECOMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 26.
SEQUENCE CHARACTERASTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-767-128-26
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Patent No. 6111079
GENERAL INPORMATION
PAPLICANT: WYLE, DWANE E.
PAPLICANT: MORRAY, PETER JOSEPH
APPLICANT: GORBEL, PETER ADSEPH
APPLICANT: MORRAY, PETER ADSEPH
APPLICANT: MURRAY, PETER ADSEPH
APPLICANT: MURRAY, PETER ADSEPH
APPLICANT: MURRAY, PETER ADSEPH
APPLICANT: MURRAY, PETER ADSEPTIONS COUNTY THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: MACCHARIT, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRANCH/DOCKET NUMBER: 05.03.08
FELEROWUNICATION INFORMATION:
FELECOMMUNICATION OF 10:
SEQUENCE (510) 655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE (TARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: protein
US-08-483-749A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTEMARE: FESTSEQ Version 1.5
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION HATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 04-DEC-1996
CLASSIFICATION OF AND ATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAMBE: CARLER, CHARTER
NAMBE: CARLER, CHARTER
NAMBE: CARLER, CHARTER
NAMBE: CARLER, CHARTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIRLKSDNYATHYAESVKG 19
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US-08-767-128-26
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Patent No. 5919452
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: GENERAC, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: METHODS OF TREATING TNF - MEDIATED DISEASE USING
TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.5%; Score 74; DB 1; Length 119; Best Local Similarity 84.2%; Pred. No. 7e-05; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLAP Compatible
COMPUTER: Patentl BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,861A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,413
APPLICATION NUMBER: US 08/013,413
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,606
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                    FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BYOOK, DAVIG B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 21,592
REFERENCE/DOCKET NUMBER: 21,592
REFERENCE/DOCKET NUMBER: 07103
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
US 07/853,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 EIRSKSINSATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-324-799-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington
STATE: Massachusetts
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02173
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US-08-192-861A-5
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Pred. No. 7e-05;
0; Mismatches 3; Indels
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Sequence 5, Application US/08324799

GENERAL INFORMATION

APPLICANT: Le, Junming

APPLICANT: Vilcek, Jan

APPLICANT: Daddona, Peter E.

APPLICANT: Knight, David M.

APPLICANT: Siegel, Scott A.

TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,799
RIING APPLICATION DATA:
APPLICATION NUMBER: 08/192,093
FILING DATE: 04-FEB-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,102
FILING DATE: 04-FEB-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,861
FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/3,413
FILING DATE: 02-FEB-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,413
FILING DATE: 02-FEB-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/010,406
FILING DATE: 02-FEB-1993
RIOR APPLICATION NUMBER: US/08/010,406
TELLING DATE: 18-MAR-1991
ATTORNEY/AGENT THORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REPERENCE/DOCKET NUMBER: NYU93-01M3
TELECHONE: (617) 861-6240
TELEPAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-192-102-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02173
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75.5%; Score 74; DB 4; Length 119; 84.2%; Pred. No. 7e-05; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 16; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Might, David M.
APPLICANT: Siegel, Socht A.
TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Lexington

STATE: Lexington

STATE: Massachusetts

COMPUTER: Massachusetts

COMPUTER: Lexington

COMPUTER: STATE: FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: STATEM: PC-DOS/MS-DOS

SOFTWARE: PAETELINE Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/133,119

FILING DATE: 11-DEC-1995

PRIOR APPLICATION NUMBER: 08/570,674

FILING DATE: 18-OCT-1994

PRIOR APPLICATION NUMBER: 08/324,799

FILING DATE: 04-FEB-1994

PRIOR APPLICATION NUMBER: 08/192,093

FILING DATE: 04-FEB-1994

PRIOR APPLICATION NUMBER: 08/192,102

FILING DATE: 04-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 0.1M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEPHONE: (781) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATE: 08/192,861
PRIOR APPLICATION DATE: APPLICATION NUMBER: US 08/013,413
FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATE: APPLICATION NUMBER: US 08/010 405
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; Sequence 5, Application US/09133119
; Patent No. 6277969
; GENERAL INFORMATION:
APPLICANT: Le, Juuming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 EIRSKSINSATHYAESVKG 68
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PILING DATE: 29-JAN-1993

PRIOR APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US 07/943,852
PRIOR APPLICATION DATA:
PILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REPERENCI-DOCCHET NUMBER: NYU93-01M4A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-133-119-5
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR EEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Gaps

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Appli Appli Appli Appli

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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-278-0400
                                                                                                                                                                                                                                                                      Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INFOATION:
APPLICANT: Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDED ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
       US-09-130-783-33
US-08-483-749A-16
PCT-US93-1611-5
US-08-253-877C-10
US-08-253-677C-10
US-08-452-164A-10
US-08-603-024-4
US-08-603-024-4
US-08-603-024-27
PCT-US93-11611-2
PCT-US93-11611-2
PCT-US93-11611-2
US-08-211-677-10
US-09-511-477-10
US-09-511-477-10
US-09-511-507-10
US-09-511-677-10
US-09-511-677-10
US-09-511-677-10
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                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper and Dunham LLP STRET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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98, Appli
108, Appl
108, Appl
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97, Appli
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                                                                     April 22, 2003, 12:48:49 % Search time 7.875 Seconds (without alignments) 33.626 Million cell updates/sec
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/cgn2 6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2 6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/jaa/PcTUS COMB.pep:*
/cgn2 6/ptodata/1/jaa/PcTUS COMB.pep:*
         GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-672_345C-27
US-09-214-095D-27
US-08-672-345C-8
US-08-672-345C-8
US-08-672-345C-98
US-09-214-095D-108
US-09-214-095D-1108
US-09-214-095D-21
US-08-672-345C-5
US-08-672-345C-95
US-08-672-345C-95
US-08-672-345C-95
US-08-672-345C-97
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-112
US-09-214-095D-113
US-08-438-123-3
US-08-438-123-3
US-08-438-123-3
US-08-438-123-1
US-08-468-661-3
US-08-468-661-3
US-08-468-661-3
US-08-468-661-3
US-08-468-661-3
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                 - protein search, using sw model
                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                Issued Patents AA:*
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                                 US-09-674-716B-7
48
1 QQLVEYPFT 9
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Match Length
                Copyright
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Maximum DB 8
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                                                                                                                                      Sequence:
                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                Database
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Gaps

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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Murinae gen. sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 QQFVEYPFT 102
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                                                            US-08-672-345C-98
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88.9%; Pred. No. 0.16;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         Score 44; DB 4; Length 9;
Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08672345C
| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. |
| TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY INVERES OF SEQUENCES: 108 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York STATE: New York STATE: New York
US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280897
; GENERAL INFORMATION:
; AFPLICATION:
; TITLE OP INVENTION:
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 27
; SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE: 1,003

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UUN-1996
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REBERBENGE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-279-0400
TELEFRAX: 212-279-0400
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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88.9%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Matches 8; Conservative
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-672-345C-8
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Pred. No. 1.9e+05;
1; Mismatches 2; Indels
   66.7%; Pred. No. 1.9e+05;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09214095D
Fatent No. 6280907
GENERAL INFORMATION:
APPLICANT: Landry, Donald
ITILE OF INVENTION:
CURRENT APPLICANT: 51400-A-PCT-US
CURRENT FAILING DATE: 1999-07-19
CURRENT FILING DATE: 1999-07-19
SOFTWARE: Patentin version 3.0
SSEQ ID NOS: 121
SEQ ID NO 21
LENGTH: 9
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COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 24.0N-1996
CIRRENT APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24.0N-1996
CLASSIFICATION HORBER: US/08/672,345C
FILING DATE: 24.0N-1996
CLASSIFICATION WINBER: 05/75/51400
FRETERRENES/DOCKET NUMBER: 05/75/51400
FRETERRENES/DOCKET NUMBER: 05/75/51400
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-739-0400
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-739-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FENTALE TILL AMONG THE TILL AMONG THE
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Patent No. 5548658
GENERAL INFORMATION:
APPLICANT Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
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1185 Avenue of the Americas
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murinae gen.sp
Best Local Similarity
Matches 6; Conserv
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STATE: New York
                                                                                            1 QOLVEYPFT 9
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1 QHFVDYPFT 9
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US-08-672-345C-5
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Pred. No. 0.16;
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Sequence 21, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                 Sequence 108, Application US/09214095D
Patent No. 6280987;
GERREAL INFORMATION:
APPLICANT: Landry. Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFRENCE: 51400-A-PCT-US
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 113
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MEDIUM TYPE: Flopyy disk
COMPUTER: IRM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
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88.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.7
Best Local Similarity 88.5
Matches 8; Conservative
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; MOLECULE TYPE: peptide
US-08-672-345C-21
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STRANDEDNESS: sin
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                                                  94 QOFVEYPFT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-108
                                                                                                                                           RESULT 6
US-09-214-095D-108
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MOLECULE TYPE: protein US-08-672-345C-95
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CITY: New York
STATE: New York
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94 QHFVDYPFT 102
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    COUNTRY:
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                                    75.0%; Score 36; DB 2; Length 113; 66.7%; Pred. No. 5.6; 2; Indels tive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentln Release #1.0, Version #1.30
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLESSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLESSIFICATION NUMBER: 28,678
FEFERENCE/DOCKET NUMBER: 0575/51400
FELEFAX: 212-278-0400
FELEFAX: 212-319-0525
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FEMALE: FEMALE: 113 amino acids
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US-08-672-345C-95
US-08-672-345C-95
Sequence 95, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVERTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE SADER
GENERSPONDENCE ADDRESS:
CORPER 2000 EN CAPALYTIC ANTIBODY
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                      Sequence 7, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                 Query Match
Best Local Similarity 66...,
Endes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 113 amino acids TYPE: amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                              | |:||||
94 QHFVDYPFT 102
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94 QHFVDYPFT 102
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STATE: New York
                                                                                                                       1 QQLVEYPFT 9
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US-08-672-345C-7
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US-08-672-345C-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.0%; Score 36; DB 4; Length 113; Best Local Similarity 66.7%; Pred. No. 5.6; Matches 6; Conservative 1; Mismatches 2; Indels
                                                    Score 36; DB 2; Length 113;
Pred. No. 5.6;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                    RESULT 13
US-09-214-095D-5
Sequence 5, Application US/09214095D
Sequence 10. Application US/09214095D
Sequence 10. Application US/09214095D
Sequence 10. Application US/09214095D
SERVERAL INFORMATION:
SETILE OF INVENTION:
STILE REFERENCE: 51400-A-PCT-US
CURRENT FAPLICATION NUMBER: US/09/214,095D
SURRENT FILIAG DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 51400-A-PCT-US
CURRENT PILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-14-095D-100
Sequence 100, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICAM: LANGLY, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09214095D Patent No. 6280987 GENERAL INFORMATION:
                                                           Query Match 75.0%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Murinae gen. sp
US-09-214-095D-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Murinae gen. Sp.
US-09-214-095D-5
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQLVEYPFT 9
| |:||||
94 QHFVDYPFT 102
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US-08-672-345C-97
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; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 199-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-100

Query Match
US-09-214-095D-100

Query Match

QUIVEYPET 9

QUIVEYPET 9

QV 1 QQIVEYPET 9

QV 1 QQIVEYPET 9

QV 1 QQIVEYPET 9

QV 1 QQIVEYPET 102

Search completed: April 22, 2003, 12:55:41
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Sequence 6, Appli
Sequence 95, Appl
Sequence 96, Appl
Sequence 97, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 8, Appli
Sequence 98, Appl
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Seguence 25, App]
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                 April 22, 2003, 12:48:49; Search time 14 Seconds (without alignments) 33.626 Million cell updates/sec
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Sequence 43, Al
Sequence 79, Al
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Sequence 104,
Sequence 112,
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*
                 GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-214-095D-22
US-09-214-095D-22
US-09-214-095D-22
US-08-672-345C-8
US-08-672-345C-8
US-08-672-345C-9
US-08-672-345C-19
US-08-214-095D-108
US-08-214-095D-108
US-08-214-095D-19
US-08-672-345C-5
US-08-672-345C-6
US-08-672-345C-9
US-08-214-095D-100
US-09-214-095D-104
US-09-214-095D-104
US-09-214-095D-104
US-09-214-095D-105
US-09-214-095D-105
US-09-214-095D-105
US-09-214-095D-119
US-09-214-095D-119
US-08-672-345C-3
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                         US-09-674-716B-3
81
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Match Length
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                                                                                   OM protein
                                                                                                                                                                                                                               Sequence:
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                                                                                                                         Run on:
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No.
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Sequence 8
Sequence 8
Sequence 8
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Landary Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDER AND TESS:
ADDRESSEE: Cooper and Dunham Lip-
STREFT: 1185 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: TO 36
COWUTRY: USA
STATE: PROPPY disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PRACHAILE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PATCHION DATE:
COMPUTER: PATCHION DATE:
COMPUTER: PATCHION THESE
SOFTWARE: PATCHION THESE
COMPUTER: PATCHION THESE
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 212-310-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
LENGTH: amino acids
US-09-214-095D-43
US-09-214-095D-19
US-09-214-095D-116
US-08-672-345C-9
US-08-672-345C-99
US-08-672-345C-99
US-08-477-877B-89
US-08-477-877B-89
US-08-477-877B-89
US-08-477-998B-89
US-08-477-998B-89
US-08-477-998B-89
US-08-477-878-87
US-08-890-011-6
US-08-890-011-6
US-08-893-0135A-38
US-08-983-0135A-38
US-08-477-877B-87
US-08-477-877B-87
US-08-477-877B-87
US-08-477-877B-87
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93.8%;
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Best Local Similarity 93.0,
These 15; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-672-345C-8

US-08-672-345C-8

Sequence 8, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:
APPLICANT:
INFORMATION:
APPLICANT:
APPLICANTS:
ADDRESSEE:
Cooper and bunham LLP
STREET: 1185 Avenue of the Americas
CONTRY: New York
COUNTRY: USA
ZIP: 1003 Avenue of the Americas
COMPUTRY: USA
ZIP: 1003 Avenue of the Americas
COMPUTRY: USA
ZIP: 1004 York
COMPUTRY: USA
ZIP: 1004 Avenue of the Americas
COMPUTRY: USA
ZIP: 1005 Avenue of the Americas
COMPUTRY: USA
ZIP: 1004 Avenue of the Americas
COMPUTRY: USA
ZIP: 1004 Avenue of the Americas
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COMPUTRY: USA
ZIP: 1004 Avenue of the Americas
COMPUTRY: USA
ZIP: 1005 Avenue of the Americas
COMPUTRY: USA
ZIP: 1006 Avenue of the Americas
COMPUTRY: USA
ZIP: 1007 Avenue of the Americas
COMPUTRY: USA
                                           US-09-214-095D-25

US-09-214-095D-25

Sequence 25, Application US/09214095D

Patent No. 6280387

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQ 1D NOS:

NUMBER OF SEQ 1D NOS:

SOFTWARE:

Patent In version 3.0

BRO 1D NO 25

LENGTH: 16
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-25
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-672-345C-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.1%; Score 77; DB 2; Length 16; 93.8%; Pred. No. 1.3e-06; tive 1; Mismatches 0; Indels
         Sequence 25, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
UG-09-214-095D-22
Sequence 22, Application US/09214095D
Fatent No. 6280987
CENERAL INFORMATION:
PAPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT PILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 0575/51400

TELECOMMUNICATION:

TELECOMMUNICATION:

TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 25:
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-22
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Best Local Similarity 93.8
Matches 15; Conservative
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-672-345C-25
US-08-672-345C-25
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LENGTH: 16
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Pred. No. 9.9e-06;
                                                         Indels
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### Patent No. 6280987
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ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CITY: New York
STATE: New York
COMPUTR: New York
COMPUTR: EADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READDABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: EADDABLE FORM:
MEDIUM TYPE: PATENTIN PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UN-1996
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
FREFERENCY DOCKET NUMBER: 0575/51400
TELEFRAN: 212-278-0400
TELEFRAN: 212-391-0525
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
INFORMATION COID
STRANDENNESS: SINGLE
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US-08-672-345C-19
US-08-672-345C
Sequence 19, Application US/08672345C
Patent No. 5946658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                       Pred. No. 9.9e-06;
1; Mismatches 0;
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             Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 93.8%;
Matches 15; Conservative
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; ORGANISM: Murine
US-09-214-095D-108
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Pred. No. 9.9e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                     Sequence 98, Application US/08672345C
Patent No. 5548658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
ITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSED:
CORRESPONDENCE TOOPER and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: ElbM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLIASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 0575/51400

TELEPRONE 12-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: alingle

MINECHTER TONE: AND ADDEDNESS: alingle

STRANDEDNESS: alingle
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APPLICANT: Landry, Donald
TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOPTWARE: Patentin version 3.0
LENGTH: 113
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Patent No. 6280987
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93.8%;
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1 RSSKSLLYKDGKTYLN 16
                                 24 RSSKSLLYEDGKTYLN 39
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ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSSKSLLYKDGKTYLN 16
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; MOLECULE TYPE: peptide
US-08-672-345C-98
                                                                                                                                                                                      US-08-672-345C-98
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COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFTCATION NUMBER: 05.5/51400
FILING DATE: JOHN PS.
REFERENCE/DOCKET NUMBER: 05.5/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:
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Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-COCAINE CATALYTIC ANTIBODY
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87.5%; Pred. No. 2.8e-06;
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Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-214-095D-28
Sequence 28, Application US/09214095D
Parent No. 6280987
GENERAL INFORMATION:
TAPPLICANT: Landry, Donald
TILE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION UNMERE: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQUENCE 16
                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                      Query Match 92.6%;
Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Murinae gen. sp.
                     ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-19
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Pred. No. 2.8e-06;
2; Mismatches 0; Indels
                                                  Score 75; DB 2; Length 16;
Pred. No. 2.8e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            | Sequence 28, Application US/08672345C |
| Sequence 28, Application US/08672345C |
| Patent No. 5948658 |
| GENERAL INFORMATION: APPLICANT: Landry Donald, W. APPLICANT: Landry Donald, W. NUMBER OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Cooper and Dunham LLP |
| STREET: 1185 Avenue of the Americaf |
| CITY: New York |
| COUNTRY: USA |
| COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
DEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUM-1996
CLASSIFICATION: 435
ATTOMNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELEPHONE: 212-278-0400
TELEPHONE: 212-39-0525
INFORMATION POR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
TENDATH: 16 amino acids
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Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
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                                                     Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-28
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US-08-672-345C-19
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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TELECOMMUTCATION INFORMATION:
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APPLICANT: Landry Donald, W.
TITLE OF INVENTION: AWTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                                                                                                                                     Score 75; DB 2;
Pred. No. 2.1e-05;
                                                                                                                                                                                                           2; Mismatches
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; Sequence 6, Application US/08672345C
; Patent No. 5948658
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
                                                                                                                                                                   92.6%;
87.5%;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-5
                                                                                                                                                               Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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Matches 14; Conservative
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; MOLECULE TYPE: protein
US-08-672-345C-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION WHOMER: 28,678
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELEFANICALORET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANICALORET JOHN P.
TELEFANICALORET J
                                                                                                                                                                  STREET: 1185 Avenue of the Americas
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and D
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Best Local Similarity 87.5
Matches 14; Conservative
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; Sequence 23, Application US/08672345C
; Patent No. 5948658
; Patent No. 5948658
; Patent No. 5948658
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; WUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; COUNTRY: New York
; STATE: New York
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COUNTRY: DO...

ZIP: 10036
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UNV-1996
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: White, John P.
RESTRACTON NUMBER: 28,678
RESTRACTON NUMBER: 28,678
RESTRACTON NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMU
                  US-08-963-825-18

US-09-50-811-18

US-09-540-608-18

US-09-548-608-18

US-09-589-578-9

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US-09-188-936-336

US-09-188-936-336

US-09-188-948-5

US-09-029-348-5

US-09-029-348-5

US-09-029-348-4

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LMSTRAS 7
  RESULT
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                             April 22, 2003, 12:48:49; Search time 6.125 Seconds (without alignments) 33.626 Million cell updates/sec
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(Sgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Sgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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(Sgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Sgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                  GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-214-095D-23
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US-08-672-345C-6
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US-08-672-345C-96
US-08-672-345C-96
US-08-672-345C-96
US-08-672-345C-96
US-09-214-095D-108
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US-09-214-095D-108
US-09-214-095D-108
US-09-214-095D-108
US-09-214-095D-20
US-08-672-345C-5
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US-09-214-095D-80
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                                                                                                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                                     Copyright
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                                                                                                                                                                                                                                                                   Perfect score:
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Maximum DB
                                                                                                       OM protein
                                                                                                                                                                                                                                                                                             Sequence:
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Query Match 100.0%; Score 31; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 1.9e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Sequence 23, Application US/09214095D
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 23
; LENGRH: 7
; LENGRH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09214095D
Farent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANT-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-4-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER: OF SEQ ID NOS: 121
SEQ ID NO 26
SEQ ID NO 26
     NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-23
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-26
                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||
1 LMSTRAS 7
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Sequence 29, Application US/08672345C

Sequence 29, Application US/08672345C

SEQUENCE 20: Sequence 29: Application US/08672345C

TOTALE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

STREET: New York

STATE: New York
                                                                                                                                                                                                                                                                                                          CUMPUTATE USAN

CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIPICATION: 435

ATTORNEY AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UGA

ZIP: 10036

ZIP: 10036

COUNTRY: UGA

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-UN-1996

CLASSIFICATION: 435

ATTORNEX/AGENT INFORMATION:
US-08-672-345C-26
; Sequence 26, Application US/08672345C
; Patent No. 594868
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; CORRESPONDENCES: 108
; CORRESPONDENCE ADDRESS:
; COOPER and Dunham LLP
; STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 31; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
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Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches
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New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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55 LMSTRAS 61
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: 28,678
FREASIFIATION NUMBER: 28,678
FREGISTRATION INFORMATION:
FELEPHONE: 212-278-0400
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-378-0400
FELEFAX: 212-378-0400
FELEFAX: 212-378-0400
FELEFAX: 212-378-0400
FELEFAX: 212-378-0400
FELEFAX: 213-31-0525
FUNDORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SUPPLICES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                     Sequence 29, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FLILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 4; I
100.0%; Pred. No. 1.9e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08672345C Patent No. 5948658
                                                                                                                                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Murinae gen. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LMSTRAS 7
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                                                                                                              US-09-214-095D-29
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                                                                                                                                                                                                                                                                                                                     SOFTWARE:
SEQ ID NO 29
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DB 2; Length 113;

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Sequence 7. Application US/08672345C

Patent No. 554865B

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMULCATION INFORMATION:
TELEFRAM: 212-278-0400
TELEFRAM: 212-39-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 31; DB 2;
100.0%; Pred. No. 1.3;
tive 0; Mismatches 0
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COMPUTER READABLE FORM:
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   Query Match 100.0%; Score 31; DB 2; Length 113; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           US-US-1/2-345C-9/)

| Sequence 97: Application US/08672345C |
| Patent No. 5348658 |
| GENERAL INFORMATION: ANTI-COCAINE CATALYTIC ANTIBODY TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108 |
| CORRESPONDENCE ADDRESS: 108 |
| CORRESPONDENCE ADDRESS: 108 |
| CORRESPONDENCE ADDRESS: 108 |
| STREET: 1185 Avenue of the Americas CITY: New York STRATE: New York COUNTRY: USA |
| COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98 Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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US-08-672-345C-98
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US-08-672-345C-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIREE:: LIBS AVENUE OF THE AMERICAS SIREE:: LIBS AVENUE OF THE AMERICAS STATE: New York COUNTRY: USA ZIP: 10036
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 RESISTRATION NUMBER: 28,678 RESISTRATION NUMBER: 0575/51400 TELEBENOME: 212-278-9400
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
GOMPUTER: IBM PC Compatible
GOMPUTER: IBM PC Compatible
GOMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRENCE/DOCKET NUMBER: 28,678
REFERRENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 8:
CENGTH: 113 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MULECULE TYPE: protein
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Sequence 96, Application US/08672345C

Sequence 96, Application US/08672345C

GENERAL NO. 59486D0:

GENERAL LANGEMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas
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INFORMATION FOR SEQ ID NO: 96.
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; OKGANISM: Murinae gen. sp
US-09-214-095D-7
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55 LMSTRAS 61
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US-09-214-095D-8
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APPLICANT: Landry, Donald; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; TITLE REFERENCE: 51400-A-PCT-US; CURRENT APPLICATION NUMBER: US/09/214,095D; CURRENT FILING DATE: 1999-07-19; NUMBER OF SEQ ID NOS: 121; SOFTWARE: Patentin version 3.0; SEQ ID NO 6; SEQ ID N
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AMINERS.
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Patent No. 6280997
GRENEAL INFORMATION:
APPLICANT: Landry, Donald
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-6
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US-09-214-095D-7
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